Package ‘MetaGxOvarian’

December 26, 2024

Type Package

Title Transcriptomic Ovarian Cancer Datasets

Version 1.26.0

Date `r Sys.date()`

Description A collection of Ovarian Cancer Transcriptomic Datasets that are part of the MetaGxData package compendium.

License Artistic-2.0

Depends Biobase, AnnotationHub, ExperimentHub, SummarizedExperiment, R (>= 3.6.0)

Imports stats, lattice, impute

Suggests testthat, xtable, rmarkdown, knitr, BiocStyle, markdown

Encoding UTF-8

VignetteBuilder knitr

NeedsCompilation no

biocViews ExpressionData, ExperimentHub, CancerData, Homo_sapiens_Data, ArrayExpress, GEO, NCI, MicroarrayData, ExperimentData

LazyData yes

RoxygenNote 7.1.1

git_url https://git.bioconductor.org/packages/MetaGxOvarian

git_branch RELEASE_3_20

git_last_commit 01219ab

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Repository Bioconductor 3.20

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Contents

`attention` *days_to_death*

Description

This is a note to inform package users that the days_to_death variable is also valid for living pateints. In this case, the value in days_to_death is the number of days since the last follow-up appointment.

Format

A field included in various data files in the this package.

`duplicates` *a list containing the names of patients that are believed to be dulicates across datasets*

Description

The object is a list where each element is a patient ID that is believed to be a duplicate of a patient in another dataset. Patients are designated as duplicated if they have Spearman correlations greater than or equal to 0.98 with other patient expression profiles

Format

A list with 130 elements, each of which is a patient ID.

`E.MTAB.386` *Angiogenic mRNA and microRNA gene expression signature predicts a novel subtype of serous ovarian cancer.*

Description

Ovarian cancer is the fifth leading cause of cancer death for women in the U.S. and the seventh most fatal worldwide. Although ovarian cancer is notable for its initial sensitivity to platinum-based therapies, the vast majority of patients eventually develop recurrent cancer and succumb to increasingly platinum-resistant disease. Modern, targeted cancer drugs intervene in cell signaling, and identifying key disease mechanisms and pathways would greatly advance our treatment abilities. In order to shed light on the molecular diversity of ovarian cancer, we performed comprehensive transcriptional profiling on 129 advanced stage, high grade serous ovarian cancers. We implemented a, re-sampling based version of the ISIS class discovery algorithm (rISIS: robust ISIS) and applied it to the entire set of ovarian cancer transcriptional profiles. rISIS identified a previously undescribed patient stratification, further supported by micro-RNA expression profiles, and gene set enrichment analysis found strong biological support for the stratification by extracellular matrix, cell adhesion, and angiogenesis genes. The corresponding "angiogenesis signature" was validated in ten published independent ovarian cancer gene expression datasets and is significantly associated with overall survival. The subtypes we have defined are of potential translational interest as they may be relevant for identifying patients who may benefit from the addition of anti-angiogenic therapies that are now being tested in clinical trials.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Bentink S, Haibe-Kains B, Risch T, Fan J-B, Hirsch MS, Holt
  Laboratory: Bentink, Matulonis 2012
  Contact information:
  Title: Angiogenic mRNA and microRNA gene expression signature predicts a novel
  URL:
  PMIDs: 22348002

  Abstract: A 212 word abstract is available. Use 'abstract' method.
```

```
    Information is available on: preprocessing
    notes:
     platform_title:
        Illumina humanRef-8 v2.0 expression beadchip
     platform_shorttitle:
        Illumina humanRef-8 v2.0
     platform_summary:
        illuminaHumanv2
     platform_manufacturer:
        Illumina
     platform_distribution:
        commercial
     platform_accession:
        GPL6104
     version:
        2015-09-22 19:06:44

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: ILMN_1343291 ILMN_1651228 ... ILMN_1815951 (12449
    total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 12449 features, 129 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

      n  events  median 0.95LCL 0.95UCL
 129.00   73.00    3.51    2.68    4.13

---------------------------
Available sample meta-data:
---------------------------

unique_patient_ID:
  DFCI.1  DFCI.10 DFCI.100 DFCI.101 DFCI.102 DFCI.103 DFCI.104 DFCI.105
       1        1        1        1        1        1        1        1
DFCI.106 DFCI.107 DFCI.108 DFCI.109  DFCI.11 DFCI.110 DFCI.111 DFCI.112
       1        1        1        1        1        1        1        1
DFCI.113 DFCI.114 DFCI.115 DFCI.116 DFCI.117 DFCI.118 DFCI.119  DFCI.12
       1        1        1        1        1        1        1        1
DFCI.120 DFCI.121 DFCI.122 DFCI.123 DFCI.124 DFCI.125 DFCI.126 DFCI.127
       1        1        1        1        1        1        1        1
DFCI.128 DFCI.129  DFCI.13 DFCI.130 DFCI.131 DFCI.132  DFCI.14  DFCI.15
       1        1        1        1        1        1        1        1
 DFCI.16  DFCI.17  DFCI.18  DFCI.19   DFCI.2  DFCI.20  DFCI.21  DFCI.22
       1        1        1        1        1        1        1        1
 DFCI.23  DFCI.24  DFCI.25  DFCI.26  DFCI.27  DFCI.28  DFCI.29   DFCI.3
```

```
      1        1        1        1        1        1        1        1
 DFCI.30  DFCI.31  DFCI.32  DFCI.33  DFCI.34  DFCI.35  DFCI.36  DFCI.37
      1        1        1        1        1        1        1        1
 DFCI.38  DFCI.39   DFCI.4  DFCI.40  DFCI.41  DFCI.42  DFCI.44  DFCI.45
      1        1        1        1        1        1        1        1
 DFCI.46  DFCI.47  DFCI.48  DFCI.49  DFCI.50  DFCI.51  DFCI.52  DFCI.53
      1        1        1        1        1        1        1        1
 DFCI.54  DFCI.55  DFCI.56  DFCI.57  DFCI.58  DFCI.59   DFCI.6  DFCI.60
      1        1        1        1        1        1        1        1
 DFCI.61  DFCI.62  DFCI.63  DFCI.64  DFCI.65  DFCI.66  DFCI.67  DFCI.68
      1        1        1        1        1        1        1        1
 DFCI.69   DFCI.7  DFCI.70  (Other)
      1        1        1       30

sample_type:
tumor
  129

histological_type:
ser
129

primarysite:
 ov
129

summarygrade:
high
 129

summarystage:
early  late
    1   128

tumorstage:
  2   3   4
  1 109  19

substage:
   a    b    c NA's
   5   12   93   19

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  21.00   50.00   66.00   60.71   72.00   95.00

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    3.9   516.9   917.1  1007.0  1401.0  2724.0

vital_status:
deceased   living
```

```
      73       56

debulking:
   optimal suboptimal       NA's
        98         28          3

uncurated_author_metadata:
                                                         Source.Name: DFCI-100//

                                                                 Source.Name: DF

                                                                Source.Name: DFC

                                                           Source.Name: DFCI-103

                                                          Source.Name: DFCI-104/

                                                         Source.Name: DFCI-105//

                                                          Source.Name: DFCI-106/

                                                          Source.Name: DFCI-107/

                                                           Source.Name: DFCI-108

                                                         Source.Name: DFCI-109//

                                                              Source.Name: DFCI-

                                                            Source.Name: DFCI-11

                                                         Source.Name: DFCI-111//

                                                           Source.Name: DFCI-112

                                                           Source.Name: DFCI-113

                                                               Source.Name: DFCI

                                                          Source.Name: DFCI-115/

                                                         Source.Name: DFCI-116//

                                                            Source.Name: DFCI-11

Source.Name: DFCI-118///Characteristics.Age.: Age <has_measurement <Measurement

                                                           Source.Name: DFCI-119

                                                            Source.Name: DFCI-11

   Source.Name: DFCI-120///Characteristics.Age.: Age <has_measurement <Measureme
```

Source.Name: DFCI-12

Source.Name: DFCI

Source.Name: DFCI-123/

Source.Name: DFCI-12

Source.Name: DFCI-1

Source.Name: DFC

Source.Name: DFCI-127///Characteristics.Age.: Age <has_measurement <Measure

Source.Name: DFCI-12

Source.Name: DFCI-129///Characteristics.Age.: Age <has_measurement <Measureme

Source.Name: DFCI-1

Source.Name: DFCI-130///Characteristics.Age.: Age <has_measurement <Measurement

Source.Name: DFCI-131///Characteristics.Age.: Age <has_measurement <Measur

Source.Name: DFCI-132///Characteristics.Age.: Age <has_measurement <Measurement

Source.Name: DFCI-1

Source.Name: DFCI-

Source.Name: DF

Source.Name: D

Source.Name: DFCI-1

Source.Name: DFCI-1

Source.Name: DFCI-1

Source.Name:

Source.Name: DFCI-2

Source.Name: DF

Source.Name: DFCI-22///Characteristics.Age.: Age <has_measurement <Measurem

Source.Name: DFCI-23

Source.Name: DFCI-24//

Source.Name: DFCI-25

Source.Name: DFCI

Source.Name: DFCI-2

Source.Name: DFC

Source.Name: DFCI-2

Source.Name: DFC

Source.Name: DFCI

Source.Name: DFCI-3

Source.Name: DFCI

Source.Name: DFCI-

Source.Name: DFCI-

Source.Name: DFCI-3

Source.Name: DF

Source.Name: DFCI-3

Source.Name: DFCI-38

Source.Name: DFCI-39

Source.Name: DF

Source.Name: DFCI-4

Source.Name: DFCI-

Source.Name: DFCI-

Source.Name: DFCI-

Source.Name: DF

Source.Name: DFCI-4

Source.Name: DFCI-

Source.Name: DF

Source.Name: DFCI

```
Source.Name: DF
Source.Name: DFCI-
Source.Name: DFCI-51
Source.Name: DFCI-5
Source.Name: DFCI-53
Source.Name: DFCI-54
Source.Name: DFCI-
Source.Name: DFCI-56
Source.Name: DFCI-5
Source.Name: DFCI-
Source.Name: DFCI
Source.Name: DFCI
Source.Name: DFC
Source.Name: DFCI-62///Characteristics.Age.: Age <has_measurement <Measure
Source.Name: DFC
Source.Name: DFCI
Source.Name: DFCI-65
Source.Name: DFC
Source.Name: DF
Source.Name: DFCI-6
Source.Name: DFCI-6
Source.Name:
Source.Name: DFCI-
Source.Name: DFCI
```

Value

An expression set

GSE12418 *Expression analysis of stage III serous ovarian adenocarcinoma distinguishes a sub-group of survivors.*

Description

It is difficult to predict the clinical outcome for patients with ovarian cancer. However, the use of biomarkers as additional prognostic factors may improve the outcome for these patients. In order to find novel candidate biomarkers, differences in gene expressions were analysed in 54 stage III serous ovarian adenocarcinomas with oligonucleotide microarrays containing 27,000 unique probes. The microarray data was verified with quantitative real-time polymerase chain reaction for the genes TACC1, MUC5B and PRAME. Using hierarchical cluster analysis we detected a subgroup that included 60% of the survivors. The gene expressions in tumours from patients in this sub-group of survivors were compared with the remaining tumours, and 204 genes were found to be differently expressed. We conclude that the sub-group of survivors might represent patients with favourable tumour biology and sensitivity to treatment. A selection of the 204 genes might be used as a predictive model to distinguish patients within and outside of this group. Alternative chemotherapy strategies could then be offered as first-line treatment, which may lead to improvements in the clinical outcome for these patients.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Partheen K, Levan K, Osterberg L, Horvath G.Expression anal
  Laboratory: Partheen, Horvath 2006
  Contact information:
  Title: Expression analysis of stage III serous ovarian adenocarcinoma distingu
  URL:
  PMIDs: 16996261

  Abstract: A 177 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      SWEGENE H_v2.1.1_27k
   platform_shorttitle:
      SWEGENE H_v2.1.1_27k
   platform_summary:
      PartheenMetaData
   platform_manufacturer:
      other
   platform_distribution:
      non-commercial
   platform_accession:
      GPL5886
   version:
```

```
      2015-09-22 19:07:14

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 28 29 ... 29999 (11304 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 11304 features, 54 samples
Platform type:
---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
1035LA0  1047LB 1059LB0  1177DB 1178LB0  1180DB 1186DB0   123DC 1242LC0  1274LC
      1       1       1       1       1       1       1       1       1       1
  134LC  1426LB  1487DB  1528DC  1538DC  1567DB  1568DC 1574LC0   164DC  1658DC
      1       1       1       1       1       1       1       1       1       1
 1760LB  1805DB   193DC   198DC   202DC   211DC    26DC   272DC   405LB   436DC
      1       1       1       1       1       1       1       1       1       1
  452DC   454LC   45LA0   462DB   46LB0    47DC  480DC0   489DC   505DB   541DC
      1       1       1       1       1       1       1       1       1       1
  559DC   563LA   626DC   662DC   719DC  742LC0   755LC   759DC    76DC   789DC
      1       1       1       1       1       1       1       1       1       1
   83LC  918DB0  988LC0   99LC0
      1       1       1       1

sample_type:
tumor
   54

histological_type:
ser
 54

primarysite:
ov
54

summarystage:
late
  54

tumorstage:
 3
54

substage:
 b  c
```

```
19 35

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  35.00   51.25   59.50   59.56   69.75   84.00

pltx:
 y
54

os_binary:
 long short
   20    34

debulking:
   optimal suboptimal
        13         41

uncurated_author_metadata:
title: 1035LA0///geo_accession: GSM311973///status: Public on Aug 12 2008///subm

    title: 1047LB///geo_accession: GSM311974///status: Public on Aug 12 2008///s

title: 1059LB0///geo_accession: GSM311975///status: Public on Aug 12 2008///subm

           title: 1177DB///geo_accession: GSM311976///status: Public on Aug 12 2

title: 1178LB0///geo_accession: GSM311977///status: Public on Aug 12 2008///subm

           title: 1180DB///geo_accession: GSM311978///status: Public on Aug 12 2

       title: 1186DB0///geo_accession: GSM311979///status: Public on Aug 12 2008

             title: 123DC///geo_accession: GSM311945///status: Public on Aug 12

 title: 1242LC0///geo_accession: GSM311980///status: Public on Aug 12 2008///sub

     title: 1274LC///geo_accession: GSM311981///status: Public on Aug 12 2008///

      title: 134LC///geo_accession: GSM311946///status: Public on Aug 12 2008///

    title: 1426LB///geo_accession: GSM311982///status: Public on Aug 12 2008///s

           title: 1487DB///geo_accession: GSM311983///status: Public on Aug 12 2

            title: 1528DC///geo_accession: GSM311984///status: Public on Aug 12

            title: 1538DC///geo_accession: GSM311985///status: Public on Aug 12

           title: 1567DB///geo_accession: GSM311986///status: Public on Aug 12 2

            title: 1568DC///geo_accession: GSM311987///status: Public on Aug 12
```

title: 1574LC0///geo_accession: GSM311988///status: Public on Aug 12 2008///sub

title: 164DC///geo_accession: GSM311947///status: Public on Aug 12

title: 1658DC///geo_accession: GSM311989///status: Public on Aug 12

title: 1760LB///geo_accession: GSM311990///status: Public on Aug 12 2008///s

title: 1805DB///geo_accession: GSM311991///status: Public on Aug 12 2

title: 193DC///geo_accession: GSM311948///status: Public on Aug 12

title: 198DC///geo_accession: GSM311949///status: Public on Aug 12

title: 202DC///geo_accession: GSM311950///status: Public on Aug 12

title: 211DC///geo_accession: GSM311951///status: Public on Aug 12

title: 26DC///geo_accession: GSM311938///status: Public on Aug 12

title: 272DC///geo_accession: GSM311952///status: Public on Aug 12

title: 405LB///geo_accession: GSM311953///status: Public on Aug 12 2008///s

title: 436DC///geo_accession: GSM311954///status: Public on Aug 12

title: 452DC///geo_accession: GSM311955///status: Public on Aug 12

title: 454LC///geo_accession: GSM311956///status: Public on Aug 12 2008///

title: 45LA0///geo_accession: GSM311939///status: Public on Aug 12 2008///subm

title: 462DB///geo_accession: GSM311957///status: Public on Aug 12 2

title: 46LB0///geo_accession: GSM311940///status: Public on Aug 12 2008///subm

title: 47DC///geo_accession: GSM311941///status: Public on Aug 12

title: 480DC0///geo_accession: GSM311958///status: Public on Aug 12 200

title: 489DC///geo_accession: GSM311959///status: Public on Aug 12

title: 505DB///geo_accession: GSM311960///status: Public on Aug 12 2

title: 541DC///geo_accession: GSM311961///status: Public on Aug 12

title: 559DC///geo_accession: GSM311962///status: Public on Aug 12

title: 563LA///geo_accession: GSM311963///status: Public on Aug 12 2008///s

title: 626DC///geo_accession: GSM311964///status: Public on Aug 12 title: 662DC///geo_accession: GSM311965///status: Public on Aug 12

title: 719DC///geo_accession: GSM311966///status: Public on Aug 12

title: 742LC0///geo_accession: GSM311967///status: Public on Aug 12 2008///sub

title: 755LC///geo_accession: GSM311968///status: Public on Aug 12 2008///

title: 759DC///geo_accession: GSM311969///status: Public on Aug 12

title: 76DC///geo_accession: GSM311942///status: Public on Aug 12

title: 789DC///geo_accession: GSM311970///status: Public on Aug 12

title: 83LC///geo_accession: GSM311943///status: Public on Aug 12 2008///

title: 918DB0///geo_accession: GSM311971///status: Public on Aug 12 2008

title: 988LC0///geo_accession: GSM311972///status: Public on Aug 12 2008///sub

title: 99LC0///geo_accession: GSM311944///status: Public on Aug 12 2008///sub

Value

An expression set

`GSE12470` *Gene expression profiling of advanced-stage serous ovarian cancers distinguishes novel subclasses and implicates ZEB2 in tumor progression and prognosis.*

Description

To elucidate the mechanisms of rapid progression of serous ovarian cancer, gene expression profiles from 43 ovarian cancer tissues comprising eight early stage and 35 advanced stage tissues were carried out using oligonucleotide microarrays of 18,716 genes. By non-negative matrix factorization analysis using 178 genes, which were extracted as stage-specific genes, 35 advanced stage cases were classified into two subclasses with superior (n = 17) and poor (n = 18) outcome evaluated by progression-free survival (log rank test, P = 0.03). Of the 178 stage-specific genes, 112 genes were identified as showing different expression between the two subclasses. Of the 48 genes selected for biological function by gene ontology analysis or Ingenuity Pathway Analysis, five genes (ZEB2, CDH1, LTBP2, COL16A1, and ACTA2) were extracted as candidates for prognostic factors associated with progression-free survival. The relationship between high ZEB2 or low CDH1 expression and shorter progression-free survival was validated by real-time RT-PCR experiments of 37 independent advanced stage cancer samples. ZEB2 expression was negatively correlated with CDH1 expression in advanced stage samples, whereas ZEB2 knockdown in ovarian adenocarcinoma SKOV3 cells resulted in an increase in CDH1 expression. Multivariate analysis showed that high ZEB2 expression was independently associated with poor prognosis. Furthermore, the prognostic effect of E-cadherin encoded by CDH1 was verified using immunohistochemical analysis of an independent advanced stage cancer samples set (n = 74). These findings suggest that the expression of epithelial-mesenchymal transition-related genes such as ZEB2 and CDH1 may play important roles in the invasion process of advanced stage serous ovarian cancer.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Yoshihara K, Tajima A, Komata D, Yamamoto T, Kodama S, Fuji
  Laboratory: Yoshihara, Tanaka 2009
  Contact information:
  Title: Gene expression profiling of advanced-stage serous ovarian cancers dist
  URL:
  PMIDs: 19486012

  Abstract: A 253 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      Agilent-012097 Human 1A Microarray (V2) G4110B (Feature Number version)
   platform_shorttitle:
      Agilent G4110B
   platform_summary:
      hgug4110b
   platform_manufacturer:
      Agilent
   platform_distribution:
      commercial
   platform_accession:
      GPL887
   version:
      2015-09-22 19:08:17

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 3 5 ... 22571 (15999 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 15999 features, 53 samples
Platform type:
---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
Advanced serous ovarian cancer 10 Advanced serous ovarian cancer 11
                                1                                 1
```

```
Advanced serous ovarian cancer 15 Advanced serous ovarian cancer 17
                                1                                 1
Advanced serous ovarian cancer 18  Advanced serous ovarian cancer 2
                                1                                 1
Advanced serous ovarian cancer 20 Advanced serous ovarian cancer 23
                                1                                 1
Advanced serous ovarian cancer 24 Advanced serous ovarian cancer 25
                                1                                 1
Advanced serous ovarian cancer 27 Advanced serous ovarian cancer 36
                                1                                 1
Advanced serous ovarian cancer 37 Advanced serous ovarian cancer 38
                                1                                 1
Advanced serous ovarian cancer 39 Advanced serous ovarian cancer 42
                                1                                 1
Advanced serous ovarian cancer 43 Advanced serous ovarian cancer 45
                                1                                 1
Advanced serous ovarian cancer 46 Advanced serous ovarian cancer 49
                                1                                 1
Advanced serous ovarian cancer 50 Advanced serous ovarian cancer 51
                                1                                 1
Advanced serous ovarian cancer 52 Advanced serous ovarian cancer 53
                                1                                 1
Advanced serous ovarian cancer 54 Advanced serous ovarian cancer 55
                                1                                 1
Advanced serous ovarian cancer 56 Advanced serous ovarian cancer 57
                                1                                 1
Advanced serous ovarian cancer 58  Advanced serous ovarian cancer 6
                                1                                 1
Advanced serous ovarian cancer 60 Advanced serous ovarian cancer 61
                                1                                 1
Advanced serous ovarian cancer 62 Advanced serous ovarian cancer 64
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 Advanced serous ovarian cancer 7    Early serous ovarian cancer 28
                                1                                 1
   Early serous ovarian cancer 32    Early serous ovarian cancer 33
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   Early serous ovarian cancer 35     Early serous ovarian cancer 5
                                1                                 1
   Early serous ovarian cancer 65     Early serous ovarian cancer 8
                                1                                 1
    Early serous ovarian cancer 9             Peritoneum normal 12
                                1                                 1
             Peritoneum normal 15             Peritoneum normal 16
                                1                                 1
             Peritoneum normal 18             Peritoneum normal 21
                                1                                 1
             Peritoneum normal 23              Peritoneum normal 3
                                1                                 1
             Peritoneum normal 30              Peritoneum normal 4
                                1                                 1
              Peritoneum normal 7
                                1
```

```
sample_type:
healthy   tumor
     10      43

histological_type:
 ser NA's
  43   10

primarysite:
ov
53

summarystage:
early  late  NA's
    8    35    10

tumorstage:
   1 NA's
   8   45

uncurated_author_metadata:
  title: Advanced serous ovarian cancer 10///geo_accession: GSM312155///status:

  title: Advanced serous ovarian cancer 11///geo_accession: GSM312141///status:

  title: Advanced serous ovarian cancer 15///geo_accession: GSM312156///status:

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  title: Advanced serous ovarian cancer 23///geo_accession: GSM312157///status:

  title: Advanced serous ovarian cancer 24///geo_accession: GSM312145///status:

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  title: Advanced serous ovarian cancer 27///geo_accession: GSM312158///status:

            title: Advanced serous ovarian cancer 2///geo_accession: GSM312138//

  title: Advanced serous ovarian cancer 36///geo_accession: GSM312147///status:

  title: Advanced serous ovarian cancer 37///geo_accession: GSM312148///status:

  title: Advanced serous ovarian cancer 38///geo_accession: GSM312149///status:

  title: Advanced serous ovarian cancer 39///geo_accession: GSM312159///status:
```

```
title: Advanced serous ovarian cancer 42///geo_accession: GSM312160///status:
title: Advanced serous ovarian cancer 43///geo_accession: GSM312150///status:
title: Advanced serous ovarian cancer 45///geo_accession: GSM312161///status:
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title: Advanced serous ovarian cancer 50///geo_accession: GSM312163///status:
title: Advanced serous ovarian cancer 51///geo_accession: GSM312165///status:
title: Advanced serous ovarian cancer 52///geo_accession: GSM312167///status:
title: Advanced serous ovarian cancer 53///geo_accession: GSM312168///status:
title: Advanced serous ovarian cancer 54///geo_accession: GSM312152///status:
title: Advanced serous ovarian cancer 55///geo_accession: GSM312170///status: Pu
title: Advanced serous ovarian cancer 56///geo_accession: GSM312171///status:
title: Advanced serous ovarian cancer 57///geo_accession: GSM312153///status:
title: Advanced serous ovarian cancer 58///geo_accession: GSM312172///status:
title: Advanced serous ovarian cancer 60///geo_accession: GSM312173///status:
title: Advanced serous ovarian cancer 61///geo_accession: GSM312154///status:
title: Advanced serous ovarian cancer 62///geo_accession: GSM312174///status:
title: Advanced serous ovarian cancer 64///geo_accession: GSM312175///status:
title: Advanced serous ovarian cancer 6///geo_accession: GSM312139///status
title: Advanced serous ovarian cancer 7///geo_accession: GSM312140///status
title: Early serous ovarian cancer 28///geo_accession: GSM312180///statu
title: Early serous ovarian cancer 32///geo_accession: GSM312181///statu
title: Early serous ovarian cancer 33///geo_accession: GSM312182///statu
title: Early serous ovarian cancer 35///geo_accession: GSM312183///statu
title: Early serous ovarian cancer 5///geo_accession: GSM312176///sta
title: Early serous ovarian cancer 65///geo_accession: GSM312185///statu
```

```
              title: Early serous ovarian cancer 8///geo_accession: GSM312178///sta

              title: Early serous ovarian cancer 9///geo_accession: GSM312179///sta

                                             title: Peritoneum normal 12///geo_acces

                                             title: Peritoneum normal 15///geo_acces

                                             title: Peritoneum normal 16///geo_acces

                                             title: Peritoneum normal 18///geo_acces

                                             title: Peritoneum normal 21///geo_acces

                                          title: Peritoneum normal 23///geo_accessi

                                             title: Peritoneum normal 30///geo_acces

                                                  title: Peritoneum normal 3///geo_acc

                                                  title: Peritoneum normal 4///geo_acc

                                                  title: Peritoneum normal 7///geo_acc
```

```
duplicates:
GSE12470.GSE12470_GSM312135 GSE12470.GSE12470_GSM312136
                          1                           1
GSE12470.GSE12470_GSM312145 GSE12470.GSE12470_GSM312146
                          1                           1
                       NA's
                         49
```

Value

An expression set

`GSE13876` *Survival-related profile, pathways, and transcription factors in ovarian cancer.*

Description

Ovarian cancer has a poor prognosis due to advanced stage at presentation and either intrinsic or acquired resistance to classic cytotoxic drugs such as platinum and taxoids. Recent large clinical trials with different combinations and sequences of classic cytotoxic drugs indicate that further significant improvement in prognosis by this type of drugs is not to be expected. Currently a large number of drugs, targeting dysregulated molecular pathways in cancer cells have been developed and are introduced in the clinic. A major challenge is to identify those patients who will benefit from drugs targeting these specific dysregulated pathways.The aims of our study were (1) to develop a gene expression profile associated with overall survival in advanced stage serous ovarian cancer, (2) to assess the association of pathways and transcription factors with overall survival, and (3) to validate our identified profile and pathways/transcription factors in an independent set of ovarian cancers.According to a randomized design, profiling of 157 advanced stage serous ovarian cancers was performed in duplicate using approximately 35,000 70-mer oligonucleotide microarrays. A continuous predictor of overall survival was built taking into account well-known issues in microarray analysis, such as multiple testing and overfitting. A functional class scoring analysis was utilized to assess pathways/transcription factors for their association with overall survival. The prognostic value of genes that constitute our overall survival profile was validated on a fully independent, publicly available dataset of 118 well-defined primary serous ovarian cancers. Furthermore, functional class scoring analysis was also performed on this independent dataset to assess the similarities with results from our own dataset. An 86-gene overall survival profile discriminated between patients with unfavorable and favorable prognosis (median survival, 19 versus 41 mo, respectively; permutation p-value of log-rank statistic = 0.015) and maintained its independent prognostic value in multivariate analysis. Genes that composed the overall survival profile were also able to discriminate between the two risk groups in the independent dataset. In our dataset 17/167 pathways and 13/111 transcription factors were associated with overall survival, of which 16 and 12, respectively, were confirmed in the independent dataset.Our study provides new clues to genes, pathways, and transcription factors that contribute to the clinical outcome of serous ovarian cancer and might be exploited in designing new treatment strategies.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Crijns AP, Fehrmann RS, de Jong S, Gerbens F, Meersma GJ, K
  Laboratory: Crijns, van der Zee 2009
  Contact information:
  Title: Survival-related profile, pathways, and transcription factors in ovaria
  URL:
  PMIDs: 19192944

  Abstract: A 371 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      Operon human v3 ~35K 70-mer two-color oligonucleotide microarrays
   platform_shorttitle:
      Operon v3 two-color
   platform_summary:
      OperonHumanV3
   platform_manufacturer:
      other
   platform_distribution:
      non-commercial
   platform_accession:
      GPL7759
   version:
      2015-09-22 19:11:43

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1 2 ... 37629 (20939 total)
```

```
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 20939 features, 157 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

      n  events  median 0.95LCL 0.95UCL
 157.00  113.00    2.05    1.56    2.71

---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
 151 NA's
   1  156

unique_patient_ID:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
      1      40      79      79     118     157

sample_type:
tumor
  157

histological_type:
ser
157

primarysite:
 ov
157

summarygrade:
high  low NA's
  85   59   13

summarystage:
late
 157

grade:
   1    2    3    4 NA's
  14   45   82    3   13

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  21.00   50.00   60.00   57.95   67.00   84.00
```

```
days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
     30     360     630    1100    1470    7020

vital_status:
deceased   living
     113       44

uncurated_author_metadata:




       title: Ovarian tumor sample 105 / Ovarian tumor sample 106///geo_accessic


          title: Ovarian tumor sample 10 / Ovarian tumor sample 11///geo_accessi

       title: Ovarian tumor sample 111 / Ovarian tumor sample 112///geo_accessic

       title: Ovarian tumor sample 115 / Ovarian tumor sample 117///geo_accessic






       title: Ovarian tumor sample 126 / Ovarian tumor sample 127///geo_accessic














         title: Ovarian tumor sample 13 / Ovarian tumor sample 14///geo_accessic
```

`title: Ovarian tumor sample 165 / Ovarian tumor sample 166///geo_accessio`

`title: Ovarian tumor sample 193 / Ovarian tumor sample 194///geo_accessio`

```
title: Ovarian tumor sample 230 / Ovarian tumor sample 231///geo_accessi
```

```
title: Ovarian tumor sample 237 / Ovarian tumor sample 238///geo_accessio
```

```
title: Ovarian tumor sample 250 / Ovarian tumor sample 251///geo_accession: GSM4
```

```
title: Ovarian tumor sample 258 / Ovarian tumor sample 259///geo_accessio
```

```
title: Ovarian tumor sample 273 / Ovarian tumor sample 274///geo_accession
```

```
title: Ovarian tumor sample 284 / Ovarian tumor sample 285///geo_accession
```

```
title: Ovarian tumor sample 313 / Ovarian tumor sample 314///geo_accession
```

Value

An expression set

`GSE14764` *A prognostic gene expression index in ovarian cancer - validation across different independent data sets.*

Description

Ovarian carcinoma has the highest mortality rate among gynaecological malignancies. In this project, we investigated the hypothesis that molecular markers are able to predict outcome of ovarian cancer independently of classical clinical predictors, and that these molecular markers can be validated using independent data sets. We applied a semi-supervised method for prediction of patient survival. Microarrays from a cohort of 80 ovarian carcinomas (TOC cohort) were used for the development of a predictive model, which was then evaluated in an entirely independent cohort of 118 carcinomas (Duke cohort). A 300-gene ovarian prognostic index (OPI) was generated and validated in a leave-one-out approach in the TOC cohort (Kaplan-Meier analysis, p = 0.0087). In a second validation step, the prognostic power of the OPI was confirmed in an independent data set (Duke cohort, p = 0.0063). In multivariate analysis, the OPI was independent of the post-operative residual tumour, the main clinico-pathological prognostic parameter with an adjusted hazard ratio of 6.4 (TOC cohort, CI 1.8-23.5, p = 0.0049) and 1.9 (Duke cohort, CI 1.2-3.0, p = 0.0068). We constructed a combined score of molecular data (OPI) and clinical parameters (residual tumour), which was able to define patient groups with highly significant differences in survival. The integrated analysis of gene expression data as well as residual tumour can be used for optimized assessment of the prognosis of platinum-taxol-treated ovarian cancer. As traditional treatment options are limited, this analysis may be able to optimize clinical management and to identify those patients who would be candidates for new therapeutic strategies.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Denkert C, Budczies J, Darb-Esfahani S, Gy??rffy B et al. A
  Laboratory: Denkert, Lage 2009
  Contact information:
  Title: A prognostic gene expression index in ovarian cancer - validation acros
  URL:
  PMIDs: 19294737

  Abstract: A 254 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133A] Affymetrix Human Genome U133A Array
   platform_shorttitle:
      Affymetrix HG-U133A
```

```
   platform_summary:
      hgu133a
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL96
   version:
      2015-09-22 19:13:08

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
    (20967 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 20967 features, 80 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

      n  events  median 0.95LCL 0.95UCL
  80.00   21.00    4.52    4.19      NA

---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   1.00   20.75   40.50   40.50   60.25   80.00

sample_type:
tumor
   80

histological_type:
       clearcell             endo              mix            other
               2                6                1                2
             ser undifferentiated
              68                1

primarysite:
ov
80

summarygrade:
high  low
```

```
  54   26

summarystage:
early  late
    9    71

tumorstage:
 1  2  3  4
 8  1 69  2

substage:
   a    b    c NA's
   4    6   32   38

grade:
 1  2  3
 3 23 54

recurrence_status:
norecurrence   recurrence         NA's
          50           26            4

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    210     660    1050    1011    1328    2190

vital_status:
deceased   living
      21       59

batch:
2004-09-29 2004-09-30 2004-10-01 2005-01-21 2005-01-25 2005-01-26 2005-01-28
         1          2          6          4          7          8         10
2005-03-02 2006-07-26 2006-07-27 2006-07-28 2006-08-11 2006-08-18 2006-08-19
         6          4          6          4         10          3          4
2006-08-21
         5

uncurated_author_metadata:
              title: ovarian cancer: O10///geo_accession: GSM368670///status: Pu

              title: ovarian cancer: O11///geo_accession: GSM368671///status: Pu

            title: ovarian cancer: O12///geo_accession: GSM368672///status: Publ

              title: ovarian cancer: O13///geo_accession: GSM368673///status: Pu

               title: ovarian cancer: O14///geo_accession: GSM368674///status: P

             title: ovarian cancer: O15///geo_accession: GSM368675///status: Pub

           title: ovarian cancer: O16///geo_accession: GSM368676///status: Publi
```

title: ovarian cancer: O17///geo_accession: GSM368677///status: Pu

title: ovarian cancer: O18///geo_accession: GSM368678///status: Pu

title: ovarian cancer: O19///geo_accession: GSM368679///status: Pu

title: ovarian cancer: O1///geo_accession: GSM368661///status: P

title: ovarian cancer: O20///geo_accession: GSM368680///status: P

title: ovarian cancer: O21///geo_accession: GSM368681///status: Pu

title: ovarian cancer: O22///geo_accession: GSM368682///status: Pu

title: ovarian cancer: O23///geo_accession: GSM368683///status: Pu

title: ovarian cancer: O24///geo_accession: GSM368684///status: Public

title: ovarian cancer: O25///geo_accession: GSM368685///status: Pu

title: ovarian cancer: O26///geo_accession: GSM368686///status: Public on Feb 09

title: ovarian cancer: O27///geo_accession: GSM368687///status: Publ

title: ovarian cancer: O28///geo_accession: GSM368688///status: Publ

title: ovarian cancer: O29///geo_accession: GSM368689///status: Pub

title: ovarian cancer: O2///geo_accession: GSM368662///status: Pu

title: ovarian cancer: O30///geo_accession: GSM368690///status: Pu

title: ovarian cancer: O31///geo_accession: GSM368691///status: Pu

title: ovarian cancer: O32///geo_accession: GSM368692///status: Pu

title: ovarian cancer: O33///geo_accession: GSM368693///status: P

title: ovarian cancer: O34///geo_accession: GSM368694///status: Pu

title: ovarian cancer: O35///geo_accession: GSM368695///status: Pu

title: ovarian cancer: O36///geo_accession: GSM368696///status: P

title: ovarian cancer: O37///geo_accession: GSM368697///status: P

title: ovarian cancer: O38///geo_accession: GSM368698///status: Pub

title: ovarian cancer: O39///geo_accession: GSM368699///status: Pu

title: ovarian cancer: O3///geo_accession: GSM368663///status: Public on F

```
title: ovarian cancer: O40///geo_accession: GSM368700///status: Pu
title: ovarian cancer: O41///geo_accession: GSM368701///status: P
title: ovarian cancer: O42///geo_accession: GSM368702///status: Pub
title: ovarian cancer: O43///geo_accession: GSM368703///status: Pu
title: ovarian cancer: O44///geo_accession: GSM368704///status: P
title: ovarian cancer: O45///geo_accession: GSM368705///status:
title: ovarian cancer: O46///geo_accession: GSM368706///status:
title: ovarian cancer: O47///geo_accession: GSM368707///status: P
title: ovarian cancer: O48///geo_accession: GSM368708///status:
title: ovarian cancer: O49///geo_accession: GSM368709///status: P
title: ovarian cancer: O4///geo_accession: GSM368664///status: Pu
title: ovarian cancer: O50///geo_accession: GSM368710///status: P
title: ovarian cancer: O51///geo_accession: GSM368711///status:
title: ovarian cancer: O52///geo_accession: GSM368712///status: Pu
title: ovarian cancer: O53///geo_accession: GSM368713///status:
title: ovarian cancer: O54///geo_accession: GSM368714///status: P
title: ovarian cancer: O55///geo_accession: GSM368715///status: P
title: ovarian cancer: O56///geo_accession: GSM368716///status:
title: ovarian cancer: O57///geo_accession: GSM368717///status:
title: ovarian cancer: O58///geo_accession: GSM368718///status: P
title: ovarian cancer: O59///geo_accession: GSM368719///status:
title: ovarian cancer: O5///geo_accession: GSM368665///status: Pu
title: ovarian cancer: O60///geo_accession: GSM368720///status: P
title: ovarian cancer: O61///geo_accession: GSM368721///status: P
title: ovarian cancer: O62///geo_accession: GSM368722///status: P
title: ovarian cancer: O63///geo_accession: GSM368723///status: P
```

```
                    title: ovarian cancer: O64///geo_accession: GSM368724///status: P
                    title: ovarian cancer: O65///geo_accession: GSM368725///status: P
                     title: ovarian cancer: O66///geo_accession: GSM368726///status:
                     title: ovarian cancer: O67///geo_accession: GSM368727///status:
                    title: ovarian cancer: O68///geo_accession: GSM368728///status: P
                     title: ovarian cancer: O69///geo_accession: GSM368729///status:
                     title: ovarian cancer: O6///geo_accession: GSM368666///status: P
                     title: ovarian cancer: O70///geo_accession: GSM368730///status:
                     title: ovarian cancer: O71///geo_accession: GSM368731///status:
                    title: ovarian cancer: O72///geo_accession: GSM368732///status: P
          title: ovarian cancer: O73///geo_accession: GSM368733///status: Public on F
                    title: ovarian cancer: O74///geo_accession: GSM368734///status: P
                     title: ovarian cancer: O75///geo_accession: GSM368735///status:
                    title: ovarian cancer: O76///geo_accession: GSM368736///status: P
                    title: ovarian cancer: O77///geo_accession: GSM368737///status: P
                     title: ovarian cancer: O78///geo_accession: GSM368738///status:
                     title: ovarian cancer: O79///geo_accession: GSM368739///status:
                    title: ovarian cancer: O7///geo_accession: GSM368667///status: Pu
                     title: ovarian cancer: O80///geo_accession: GSM368740///status:
                    title: ovarian cancer: O8///geo_accession: GSM368668///status: Pu
                    title: ovarian cancer: O9///geo_accession: GSM368669///status: Pu

duplicates:
GSE14764.GSE14764_GSM368667 GSE14764.GSE14764_GSM368668
                          1                           1
                       NA's
                         78
```

Value

An expression set

`GSE17260` *Gene expression profile for predicting survival in advanced-stage serous ovarian cancer across two independent datasets.*

Description

Advanced-stage ovarian cancer patients are generally treated with platinum/taxane-based chemotherapy after primary debulking surgery. However, there is a wide range of outcomes for individual patients. Therefore, the clinicopathological factors alone are insufficient for predicting prognosis. Our aim is to identify a progression-free survival (PFS)-related molecular profile for predicting survival of patients with advanced-stage serous ovarian cancer.Advanced-stage serous ovarian cancer tissues from 110 Japanese patients who underwent primary surgery and platinum/taxane-based chemotherapy were profiled using oligonucleotide microarrays. We selected 88 PFS-related genes by a univariate Cox model ($p<0.01$) and generated the prognostic index based on 88 PFS-related genes after adjustment of regression coefficients of the respective genes by ridge regression Cox model using 10-fold cross-validation. The prognostic index was independently associated with PFS time compared to other clinical factors in multivariate analysis [hazard ratio (HR), 3.72; 95% confidence interval (CI), 2.66-5.43; $p<0.0001$]. In an external dataset, multivariate analysis revealed that this prognostic index was significantly correlated with PFS time (HR, 1.54; 95% CI, 1.20-1.98; $p = 0.0008$). Furthermore, the correlation between the prognostic index and overall survival time was confirmed in the two independent external datasets (log rank test, $p = 0.0010$ and 0.0008).The prognostic ability of our index based on the 88-gene expression profile in ridge regression Cox hazard model was shown to be independent of other clinical factors in predicting cancer prognosis across two distinct datasets. Further study will be necessary to improve predictive accuracy of the prognostic index toward clinical application for evaluation of the risk of recurrence in patients with advanced-stage serous ovarian cancer.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Yoshihara K, Tajima A, Yahata T, Kodama S, Fujiwara H, Suzu
  Laboratory: Yoshihara, Tanaka 2010
  Contact information:
  Title: Gene expression profile for predicting survival in advanced-stage serou
  URL:
  PMIDs: 20300634

  Abstract: A 257 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      Agilent-012391 Whole Human Genome Oligo Microarray G4112A
   platform_shorttitle:
      Agilent G4112A
   platform_summary:
      hgug4112a
```

```
   platform_manufacturer:
      Agilent
   platform_distribution:
      commercial
   platform_accession:
      GPL6848
   version:
      2015-09-22 19:16:49

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A_23_P100001 A_23_P100011 ... A_32_P99902 (30936 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 30936 features, 110 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

      n  events  median 0.95LCL 0.95UCL
 110.00   46.00    4.44    4.03      NA

---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
 Serous ovarian cancer 10 Serous ovarian cancer 100 Serous ovarian cancer 104
                        1                         1                         1
Serous ovarian cancer 106 Serous ovarian cancer 107 Serous ovarian cancer 108
                        1                         1                         1
Serous ovarian cancer 109  Serous ovarian cancer 11 Serous ovarian cancer 110
                        1                         1                         1
Serous ovarian cancer 111 Serous ovarian cancer 112 Serous ovarian cancer 113
                        1                         1                         1
Serous ovarian cancer 114 Serous ovarian cancer 115 Serous ovarian cancer 116
                        1                         1                         1
Serous ovarian cancer 117 Serous ovarian cancer 118 Serous ovarian cancer 119
                        1                         1                         1
 Serous ovarian cancer 12 Serous ovarian cancer 120 Serous ovarian cancer 122
                        1                         1                         1
Serous ovarian cancer 123 Serous ovarian cancer 127 Serous ovarian cancer 129
                        1                         1                         1
Serous ovarian cancer 130 Serous ovarian cancer 131 Serous ovarian cancer 132
                        1                         1                         1
Serous ovarian cancer 134 Serous ovarian cancer 136 Serous ovarian cancer 137
                        1                         1                         1
Serous ovarian cancer 139 Serous ovarian cancer 140 Serous ovarian cancer 143
                        1                         1                         1
```

```
Serous ovarian cancer 144 Serous ovarian cancer 145 Serous ovarian cancer 146
                        1                         1                         1
Serous ovarian cancer 148 Serous ovarian cancer 149  Serous ovarian cancer 15
                        1                         1                         1
Serous ovarian cancer 150 Serous ovarian cancer 151 Serous ovarian cancer 154
                        1                         1                         1
Serous ovarian cancer 156 Serous ovarian cancer 157  Serous ovarian cancer 16
                        1                         1                         1
Serous ovarian cancer 160  Serous ovarian cancer 17 Serous ovarian cancer 171
                        1                         1                         1
Serous ovarian cancer 172 Serous ovarian cancer 173 Serous ovarian cancer 174
                        1                         1                         1
Serous ovarian cancer 176 Serous ovarian cancer 178  Serous ovarian cancer 18
                        1                         1                         1
Serous ovarian cancer 182 Serous ovarian cancer 183 Serous ovarian cancer 184
                        1                         1                         1
Serous ovarian cancer 185 Serous ovarian cancer 186   Serous ovarian cancer 2
                        1                         1                         1
 Serous ovarian cancer 20  Serous ovarian cancer 22  Serous ovarian cancer 23
                        1                         1                         1
 Serous ovarian cancer 25  Serous ovarian cancer 27  Serous ovarian cancer 31
                        1                         1                         1
 Serous ovarian cancer 36  Serous ovarian cancer 37  Serous ovarian cancer 38
                        1                         1                         1
  Serous ovarian cancer 4  Serous ovarian cancer 41  Serous ovarian cancer 42
                        1                         1                         1
 Serous ovarian cancer 43  Serous ovarian cancer 44  Serous ovarian cancer 45
                        1                         1                         1
 Serous ovarian cancer 49  Serous ovarian cancer 50  Serous ovarian cancer 51
                        1                         1                         1
 Serous ovarian cancer 52  Serous ovarian cancer 53  Serous ovarian cancer 54
                        1                         1                         1
 Serous ovarian cancer 55  Serous ovarian cancer 56  Serous ovarian cancer 57
                        1                         1                         1
 Serous ovarian cancer 58   Serous ovarian cancer 6  Serous ovarian cancer 60
                        1                         1                         1
 Serous ovarian cancer 61  Serous ovarian cancer 62  Serous ovarian cancer 64
                        1                         1                         1
 Serous ovarian cancer 66  Serous ovarian cancer 67  Serous ovarian cancer 68
                        1                         1                         1
 Serous ovarian cancer 69   Serous ovarian cancer 7  Serous ovarian cancer 72
                        1                         1                         1
 Serous ovarian cancer 77  Serous ovarian cancer 79  Serous ovarian cancer 80
                        1                         1                         1
                  (Other)
                       11

sample_type:
tumor
  110

histological_type:
```

```
ser
110

primarysite:
 ov
110

summarygrade:
high  low
  43   67

summarystage:
late
 110

tumorstage:
 3  4
93 17

substage:
   a    b    c NA's
   6   18   69   17

grade:
 1  2  3
26 41 43

pltx:
  y
110

tax:
  y
110

days_to_tumor_recurrence:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   30.0   285.0   510.0   673.9   870.0  2250.0

recurrence_status:
norecurrence   recurrence
          34           76

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
     30     660     915    1086    1530    2430

vital_status:
deceased   living
      46       64

debulking:
```

```
   optimal suboptimal
        57         53

uncurated_author_metadata:
                           title: Serous ovarian cancer 100///geo_accession: GS

                       title: Serous ovarian cancer 104///geo_accession: GSM432

title: Serous ovarian cancer 106///geo_accession: GSM432223///status: Public on

                       title: Serous ovarian cancer 107///geo_accession: GSM432

    title: Serous ovarian cancer 108///geo_accession: GSM432225///status: Public

 title: Serous ovarian cancer 109///geo_accession: GSM432226///status: Public on

                            title: Serous ovarian cancer 10///geo_accession: GS

title: Serous ovarian cancer 110///geo_accession: GSM432228///status: Public on

title: Serous ovarian cancer 111///geo_accession: GSM432229///status: Public on

                           title: Serous ovarian cancer 112///geo_accession: GS

                       title: Serous ovarian cancer 113///geo_accession: GSM432

                        title: Serous ovarian cancer 114///geo_accession: GSM43

                       title: Serous ovarian cancer 115///geo_accession: GSM432

                       title: Serous ovarian cancer 116///geo_accession: GSM432

                           title: Serous ovarian cancer 117///geo_accession: GS

                        title: Serous ovarian cancer 118///geo_accession: GSM43

                           title: Serous ovarian cancer 119///geo_accession: GS

                            title: Serous ovarian cancer 11///geo_accession: GS

                          title: Serous ovarian cancer 120///geo_accession: GSM

                        title: Serous ovarian cancer 122///geo_accession: GSM43

                       title: Serous ovarian cancer 123///geo_accession: GSM432

                       title: Serous ovarian cancer 127///geo_accession: GSM432

                           title: Serous ovarian cancer 129///geo_accession: GS

                             title: Serous ovarian cancer 12///geo_accession: G
```

title: Serous ovarian cancer 130///geo_accession: GSM432

title: Serous ovarian cancer 131///geo_accession: GS

title: Serous ovarian cancer 132///geo_accession: GS

title: Serous ovarian cancer 134///geo_accession: GS

title: Serous ovarian cancer 136///geo_accession: GS

title: Serous ovarian cancer 137///geo_accession: GS

title: Serous ovarian cancer 139///geo_accession: GS

title: Serous ovarian cancer 140///geo_accession: GSM4

title: Serous ovarian cancer 143///geo_accession: GSM43

title: Serous ovarian cancer 144///geo_accession: GSM4

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title: Serous ovarian cancer 176///geo_accession: GSM

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title: Serous ovarian cancer 49///geo_accession: GSM432

title: Serous ovarian cancer 4///geo_accession: GSM43

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title: Serous ovarian cancer 51///geo_accession: GSM432
   title: Serous ovarian cancer 52///geo_accession: GSM
   title: Serous ovarian cancer 53///geo_accession: GSM
    title: Serous ovarian cancer 54///geo_accession: GS
    title: Serous ovarian cancer 55///geo_accession: GS
title: Serous ovarian cancer 56///geo_accession: GSM432
    title: Serous ovarian cancer 57///geo_accession: GS
    title: Serous ovarian cancer 58///geo_accession: GS
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    title: Serous ovarian cancer 68///geo_accession: GS
    title: Serous ovarian cancer 69///geo_accession: GS
     title: Serous ovarian cancer 6///geo_accession: GS
    title: Serous ovarian cancer 72///geo_accession: GS
  title: Serous ovarian cancer 77///geo_accession: GSM4
    title: Serous ovarian cancer 79///geo_accession: GS
     title: Serous ovarian cancer 7///geo_accession: GS
title: Serous ovarian cancer 80///geo_accession: GSM432
```

Value

An expression set

`GSE18520` *A gene signature predictive for outcome in advanced ovarian cancer identifies a survival factor: microfibril-associated glycoprotein 2.*

Description

Advanced stage papillary serous tumors of the ovary are responsible for the majority of ovarian cancer deaths, yet the molecular determinants modulating patient survival are poorly characterized. Here, we identify and validate a prognostic gene expression signature correlating with survival in a series of microdissected serous ovarian tumors. Independent evaluation confirmed the association of a prognostic gene microfibril-associated glycoprotein 2 (MAGP2) with poor prognosis, whereas in vitro mechanistic analyses demonstrated its ability to prolong tumor cell survival and stimulate endothelial cell motility and survival via the alpha(V)beta(3) integrin receptor. Increased MAGP2 expression correlated with microvessel density suggesting a proangiogenic role in vivo. Thus, MAGP2 may serve as a survival-associated target.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Mok SC, Bonome T, Vathipadiekal V, Bell A, Johnson ME, Wong
  Laboratory: Mok, Birrer 2009
  Contact information:
  Title: A gene signature predictive for outcome in advanced ovarian cancer iden
  URL:
  PMIDs: 19962670

  Abstract: A 110 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
   platform_shorttitle:
      Affymetrix HG-U133Plus2
   platform_summary:
      hgu133plus2
   platform_manufacturer:
      Affymetrix|Operon
   platform_distribution:
      commercial|non-commercial
   platform_accession:
      GPL570|GPL9216
   version:
      2015-09-22 19:21:25

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
    (42447 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 42447 features, 63 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

   10 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
  53.00   41.00    2.05    1.48    3.70

---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  312.0   395.0   694.0   893.3  1040.0  2237.0

sample_type:
healthy   tumor
     10      53

histological_type:
 ser NA's
  53   10

primarysite:
ov
63

summarygrade:
high NA's
  53   10

summarystage:
late NA's
  53   10

tumorstage:
   3 NA's
  53   10

grade:
   3 NA's
  53   10

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    150     450     630    1212    1440    4500      10
```

```
vital_status:
deceased   living     NA's
      41       12       10

debulking:
optimal
     63

percent_normal_cells:
 0
63

percent_stromal_cells:
 0
63

percent_tumor_cells:
100
 63

batch:
2004-03-12 2004-04-08 2004-04-09 2004-07-20 2004-08-12 2004-08-13 2004-09-30
        20          6          9         11         10          1          6

uncurated_author_metadata:
                                                title: Normal Ovary, 2008///geo_

                                                title: Normal Ovary, 2061///geo_

                                                title: Normal Ovary, 2064///geo_

                                                title: Normal Ovary, 2085///geo_

                                                title: Normal Ovary, 2225///geo_

                                                title: Normal Ovary, 2226///geo_

                                                title: Normal Ovary, 2228///geo_

                                                title: Normal Ovary, 2230///geo_

                                                title: Normal Ovary, 2234///geo_

                                                title: Normal Ovary, 2237///geo_

title: Ovarian Tumor, 1109///geo_accession: GSM461390///status: Public on Oct 17

    title: Ovarian Tumor, 1214///geo_accession: GSM461391///status: Public on Oc

    title: Ovarian Tumor, 1231///geo_accession: GSM461367///status: Public on Oc

title: Ovarian Tumor, 1562///geo_accession: GSM461368///status: Public on Oct 17
```

title: Ovarian Tumor, 1660///geo_accession: GSM461369///status: Public on Oct 17

title: Ovarian Tumor, 1993///geo_accession: GSM461400///status: Public on Oct 17

title: Ovarian Tumor, 312///geo_accession: GSM461379///status: Public on C

title: Ovarian Tumor, 317///geo_accession: GSM461348///status: Public on Oct 17

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title: Ovarian Tumor, 324///geo_accession: GSM461373///status: Public on C

title: Ovarian Tumor, 332///geo_accession: GSM461349///status: Public on

title: Ovarian Tumor, 345///geo_accession: GSM461392///status: Public on C

title: Ovarian Tumor, 349///geo_accession: GSM461350///status: Public on Oct 17

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title: Ovarian Tumor, 410///geo_accession: GSM461356///status: Public on Oct 17

title: Ovarian Tumor, 412///geo_accession: GSM461357///status: Public on Oc

title: Ovarian Tumor, 434///geo_accession: GSM461358///status: Public on C

title: Ovarian Tumor, 443///geo_accession: GSM461377///status: Public on Oc

title: Ovarian Tumor, 461///geo_accession: GSM461394///status: Public on C

title: Ovarian Tumor, 467///geo_accession: GSM461359///status: Public on C

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      title: Ovarian Tumor, 477///geo_accession: GSM461383///status: Public on O
      title: Ovarian Tumor, 486///geo_accession: GSM461395///status: Public on O
  title: Ovarian Tumor, 629///geo_accession: GSM461360///status: Public on Oct 1
      title: Ovarian Tumor, 631///geo_accession: GSM461396///status: Public on O
      title: Ovarian Tumor, 656///geo_accession: GSM461384///status: Public on O
      title: Ovarian Tumor, 662///geo_accession: GSM461370///status: Public on O
      title: Ovarian Tumor, 692///geo_accession: GSM461397///status: Public on O
      title: Ovarian Tumor, 694///geo_accession: GSM461385///status: Public on O
      title: Ovarian Tumor, 702///geo_accession: GSM461361///status: Public on O
       title: Ovarian Tumor, 714///geo_accession: GSM461362///status: Public on
      title: Ovarian Tumor, 715///geo_accession: GSM461386///status: Public on O
      title: Ovarian Tumor, 718///geo_accession: GSM461398///status: Public on O
      title: Ovarian Tumor, 744///geo_accession: GSM461378///status: Public on O
      title: Ovarian Tumor, 765///geo_accession: GSM461363///status: Public on O
      title: Ovarian Tumor, 778///geo_accession: GSM461399///status: Public on O
      title: Ovarian Tumor, 780///geo_accession: GSM461364///status: Public on O
  title: Ovarian Tumor, 786///geo_accession: GSM461387///status: Public on Oct 1
      title: Ovarian Tumor, 794///geo_accession: GSM461388///status: Public on O
       title: Ovarian Tumor, 799///geo_accession: GSM461365///status: Public on
      title: Ovarian Tumor, 800///geo_accession: GSM461371///status: Public on O
       title: Ovarian Tumor, 872///geo_accession: GSM461366///status: Public on
  title: Ovarian Tumor, 934///geo_accession: GSM461372///status: Public on Oct 1
      title: Ovarian Tumor, 970///geo_accession: GSM461389///status: Public on O

duplicates:
                              GSE18520.GSE18520_GSM462649
                                                        1
GSE18520.GSE18520_GSM462649///GSE18520.GSE18520_GSM462650
```

```
                                          1
               GSE18520.GSE18520_GSM462650
                                          1
                                       NA's
                                         60
```

Value

An expression set

GSE19829 *Gene expression profile of BRCAness that correlates with responsiveness to chemotherapy and with outcome in patients with epithelial ovarian cancer.*

Description

To define a gene expression profile of BRCAness that correlates with chemotherapy response and outcome in epithelial ovarian cancer (EOC).A publicly available microarray data set including 61 patients with EOC with either sporadic disease or BRCA(1/2) germline mutations was used for development of the BRCAness profile. Correlation with platinum responsiveness was assessed in platinum-sensitive and platinum-resistant tumor biopsy specimens from six patients with BRCA germline mutations. Association with poly-ADP ribose polymerase (PARP) inhibitor responsiveness and with radiation-induced RAD51 foci formation (a surrogate of homologous recombination) was assessed in Capan-1 cell line clones. The BRCAness profile was validated in 70 patients enriched for sporadic disease to assess its association with outcome.The BRCAness profile accurately predicted platinum responsiveness in eight out of 10 patient-derived tumor specimens, and between PARP-inhibitor sensitivity and resistance in four out of four Capan-1 clones. [corrected] When applied to the 70 patients with sporadic disease, patients with the BRCA-like (BL) profile had improved disease-free survival (34 months v 15 months; log-rank P = .013) and overall survival (72 months v 41 months; log-rank P = .006) compared with patients with a non-BRCA-like (NBL) profile, respectively. The BRCAness profile maintained independent prognostic value in multivariate analysis, which controlled for other known clinical prognostic factors.The BRCAness profile correlates with responsiveness to platinum and PARP inhibitors and identifies a subset of sporadic patients with improved outcome. Additional evaluation of this profile as a predictive tool in patients with sporadic EOC is warranted.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Konstantinopoulos PA, Spentzos D, Karlan BY, Taniguchi T et
  Laboratory: Konstantinopoulos, Cannistra 2010 hgu95
  Contact information:
  Title: Gene expression profile of BRCAness that correlates with responsiveness
  URL:
  PMIDs: 20547991

  Abstract: A 241 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
```

```
    notes:
     platform_title:
        [HG_U95Av2] Affymetrix Human Genome U95 Version 2 Array
     platform_shorttitle:
        Affymetrix HG_U95Av2
     platform_summary:
        hgu95av2
     platform_manufacturer:
        Affymetrix
     platform_distribution:
        commercial
     platform_accession:
        GPL570|GPL8300
     version:
        2015-09-22 19:26:29

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-MurIL4_at (54253 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 54253 features, 70 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

      n  events  median 0.95LCL 0.95UCL
  70.00   40.00    3.78    2.96    5.92

---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
 Ovarian cancer_sample 1 Ovarian cancer_sample 10 Ovarian cancer_sample 11
                       1                        1                        1
Ovarian cancer_sample 12 Ovarian cancer_sample 13 Ovarian cancer_sample 14
                       1                        1                        1
Ovarian cancer_sample 15 Ovarian cancer_sample 16 Ovarian cancer_sample 17
                       1                        1                        1
Ovarian cancer_sample 18 Ovarian cancer_sample 19  Ovarian cancer_sample 2
                       1                        1                        1
Ovarian cancer_sample 20 Ovarian cancer_sample 21 Ovarian cancer_sample 22
                       1                        1                        1
Ovarian cancer_sample 23 Ovarian cancer_sample 24 Ovarian cancer_sample 25
                       1                        1                        1
Ovarian cancer_sample 26 Ovarian cancer_sample 27 Ovarian cancer_sample 28
                       1                        1                        1
Ovarian cancer_sample 29  Ovarian cancer_sample 3 Ovarian cancer_sample 30
```

```
                       1                        1                        1 
Ovarian cancer_sample 31 Ovarian cancer_sample 32 Ovarian cancer_sample 33 
                       1                        1                        1 
Ovarian cancer_sample 34 Ovarian cancer_sample 35 Ovarian cancer_sample 36 
                       1                        1                        1 
Ovarian cancer_sample 37 Ovarian cancer_sample 38 Ovarian cancer_sample 39 
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                       1                        1                        1 
Ovarian cancer_sample 42 Ovarian cancer_sample 43 Ovarian cancer_sample 44 
                       1                        1                        1 
Ovarian cancer_sample 45 Ovarian cancer_sample 46 Ovarian cancer_sample 47 
                       1                        1                        1 
Ovarian cancer_sample 48 Ovarian cancer_sample 49  Ovarian cancer_sample 5 
                       1                        1                        1 
Ovarian cancer_sample 50 Ovarian cancer_sample 51 Ovarian cancer_sample 52 
                       1                        1                        1 
Ovarian cancer_sample 53 Ovarian cancer_sample 54 Ovarian cancer_sample 55 
                       1                        1                        1 
Ovarian cancer_sample 56 Ovarian cancer_sample 57 Ovarian cancer_sample 58 
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Ovarian cancer_sample 59  Ovarian cancer_sample 6 Ovarian cancer_sample 60 
                       1                        1                        1 
Ovarian cancer_sample 61 Ovarian cancer_sample 62 Ovarian cancer_sample 63 
                       1                        1                        1 
Ovarian cancer_sample 64 Ovarian cancer_sample 65 Ovarian cancer_sample 66 
                       1                        1                        1 
Ovarian cancer_sample 67 Ovarian cancer_sample 68 Ovarian cancer_sample 69 
                       1                        1                        1 
 Ovarian cancer_sample 7 Ovarian cancer_sample 70  Ovarian cancer_sample 8 
                       1                        1                        1 
 Ovarian cancer_sample 9 
                       1 

batch:
2001-09-14 2001-12-14 2002-08-20 2003-09-09 2003-09-18 2009-08-14 
         7          4         14         13          4         28 

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
   30.0   667.5  1125.0  1170.0  1522.0  3450.0 

primarysite:
ov 
70 

sample_type:
tumor 
   70 

uncurated_author_metadata:
            title: Ovarian cancer_sample 10///geo_accession: GSM495148///status:
```

title: Ovarian cancer_sample 11///geo_accession: GSM495149///status:

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title: Ovarian cancer_sample 58///geo_accession: GSM495196///status: Public on

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             title: Ovarian cancer_sample 5///geo_accession: GSM495143///status:

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             title: Ovarian cancer_sample 6///geo_accession: GSM495144///status:

       title: Ovarian cancer_sample 70///geo_accession: GSM495208///status: Publ

                  title: Ovarian cancer_sample 7///geo_accession: GSM495145///st

             title: Ovarian cancer_sample 8///geo_accession: GSM495146///status:

              title: Ovarian cancer_sample 9///geo_accession: GSM495147///status
```

```
vital_status:
deceased   living
      40       30
```

Value

An expression set

`GSE20565` *A genomic and transcriptomic approach for a differential diagnosis between primary and secondary ovarian carcinomas in patients with a previous history of breast cancer.*

Description

The distinction between primary and secondary ovarian tumors may be challenging for pathologists. The purpose of the present work was to develop genomic and transcriptomic tools to further refine the pathological diagnosis of ovarian tumors after a previous history of breast cancer.Sixteen paired breast-ovary tumors from patients with a former diagnosis of breast cancer were collected. The genomic profiles of paired tumors were analyzed using the Affymetrix GeneChip Mapping 50 K Xba Array or Genome-Wide Human SNP Array 6.0 (for one pair), and the data were normalized with ITALICS (ITerative and Alternative normaLIzation and Copy number calling for affymetrix Snp arrays) algorithm or Partek Genomic Suite, respectively. The transcriptome of paired samples was analyzed using Affymetrix GeneChip Human Genome U133 Plus 2.0 Arrays, and the data were normalized with gc-Robust Multi-array Average (gcRMA) algorithm. A hierarchical clustering of these samples was performed, combined with a dataset of well-identified primary and secondary ovarian tumors.In 12 of the 16 paired tumors analyzed, the comparison of genomic profiles confirmed the pathological diagnosis of primary ovarian tumor (n = 5) or metastasis of breast cancer (n = 7). Among four cases with uncertain pathological diagnosis, genomic profiles were clearly distinct between the ovarian and breast tumors in two pairs, thus indicating primary ovarian carcinomas, and showed common patterns in the two others, indicating metastases from breast cancer. In all pairs, the result of the transcriptomic analysis was concordant with that of the genomic analysis.In patients with ovarian carcinoma and a previous history of breast cancer, SNP array analysis can be used to distinguish primary and secondary ovarian tumors. Transcriptomic analysis may be used when primary breast tissue specimen is not available.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Meyniel JP, Cottu PH, Decraene C, Stern MH, Couturier J, Le
  Laboratory: Meyniel, Sastre-Garau 2010
  Contact information:
  Title: A genomic and transcriptomic approach for a differential diagnosis betw
  URL:
  PMIDs: 20492709

  Abstract: A 277 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
   platform_shorttitle:
      Affymetrix HG-U133Plus2
   platform_summary:
      hgu133plus2
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL570|GPL2005|GPL6801
   version:
      2015-09-22 19:33:01

featureData(eset):
```

```
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
    (42447 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 42447 features, 140 samples
Platform type:
---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
Breast metastasis in the ovary_OC01_ARN0016 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0017 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0020 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0029 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0035 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0046 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0051 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0053 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0055 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0060 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0069 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0073 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0077 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0079 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0081 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0083 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0092 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0097 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0098 [HG-U133_Plus_2]
```

```
                                                           1
Breast metastasis in the ovary_OC01_ARN0099 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0102 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0104 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0112 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0120 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0121 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0123 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0126 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0141 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0142 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0143 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0145 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0146 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0153 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0162 [HG-U133_Plus_2]
                                                           1
Breast metastasis in the ovary_OC01_ARN0201 [HG-U133_Plus_2]
                                                           1
             Ovarian carcinoma_OC01_ARN0001 [HG-U133_Plus_2]
                                                           1
             Ovarian carcinoma_OC01_ARN0002 [HG-U133_Plus_2]
                                                           1
             Ovarian carcinoma_OC01_ARN0004 [HG-U133_Plus_2]
                                                           1
             Ovarian carcinoma_OC01_ARN0005 [HG-U133_Plus_2]
                                                           1
             Ovarian carcinoma_OC01_ARN0007 [HG-U133_Plus_2]
                                                           1
             Ovarian carcinoma_OC01_ARN0008 [HG-U133_Plus_2]
                                                           1
             Ovarian carcinoma_OC01_ARN0009 [HG-U133_Plus_2]
                                                           1
             Ovarian carcinoma_OC01_ARN0010 [HG-U133_Plus_2]
                                                           1
             Ovarian carcinoma_OC01_ARN0011 [HG-U133_Plus_2]
                                                           1
             Ovarian carcinoma_OC01_ARN0012 [HG-U133_Plus_2]
```

```
                                              1
Ovarian carcinoma_OC01_ARN0013 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0015 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0022 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0023 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0025 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0028 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0030 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0032 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0034 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0036 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0037 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0038 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0039 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0041 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0042 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0045 [HG-U133_Plus_2]
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Ovarian carcinoma_OC01_ARN0049 [HG-U133_Plus_2]
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Ovarian carcinoma_OC01_ARN0057 [HG-U133_Plus_2]
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Ovarian carcinoma_OC01_ARN0058 [HG-U133_Plus_2]
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Ovarian carcinoma_OC01_ARN0061 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0062 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0063 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0064 [HG-U133_Plus_2]
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Ovarian carcinoma_OC01_ARN0066 [HG-U133_Plus_2]
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Ovarian carcinoma_OC01_ARN0067 [HG-U133_Plus_2]
                                              1
Ovarian carcinoma_OC01_ARN0070 [HG-U133_Plus_2]
```

```
                                               1
Ovarian carcinoma_OC01_ARN0072 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0075 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0076 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0080 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0084 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0085 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0089 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0091 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0093 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0095 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0096 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0100 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0101 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0103 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0105 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0106 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0107 [HG-U133_Plus_2]
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Ovarian carcinoma_OC01_ARN0108 [HG-U133_Plus_2]
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Ovarian carcinoma_OC01_ARN0109 [HG-U133_Plus_2]
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Ovarian carcinoma_OC01_ARN0111 [HG-U133_Plus_2]
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Ovarian carcinoma_OC01_ARN0113 [HG-U133_Plus_2]
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Ovarian carcinoma_OC01_ARN0114 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0115 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0116 [HG-U133_Plus_2]
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Ovarian carcinoma_OC01_ARN0118 [HG-U133_Plus_2]
                                               1
Ovarian carcinoma_OC01_ARN0119 [HG-U133_Plus_2]
```

```
                                                           1
             Ovarian carcinoma_OC01_ARN0124 [HG-U133_Plus_2]
                                                           1
             Ovarian carcinoma_OC01_ARN0125 [HG-U133_Plus_2]
                                                           1
                                                     (Other)
                                                          41

sample_type:
tumor
  140

histological_type:
clearcell      endo  mucinous     other       ser      NA's
        6         6         7         6        71        44

primarysite:
other    ov
   44    96

summarygrade:
high  low NA's
  63   33   44

summarystage:
early  late  NA's
   27    67    46

tumorstage:
   1    2    3    4 NA's
  18    9   52   15   46

substage:
   a    b    c NA's
  14   10   55   61

grade:
   1    2    3 NA's
   6   27   63   44

batch:
2006-06-01 2006-06-27 2006-06-28 2006-06-29 2006-06-30 2006-07-20 2008-03-06
        21         18         37         20         36          7          1

uncurated_author_metadata:
title: Breast metastasis in the ovary_OC01_ARN0016 [HG-U133_Plus_2]///geo_access

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title: Breast metastasis in the ovary_OC01_ARN0020 [HG-U133_Plus_2]///geo_access

title: Breast metastasis in the ovary_OC01_ARN0029 [HG-U133_Plus_2]///geo_access
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title: Breast metastasis in the ovary_OC01_ARN0035 [HG-U133_Plus_2]///geo_access
title: Breast metastasis in the ovary_OC01_ARN0046 [HG-U133_Plus_2]///geo_access
title: Breast metastasis in the ovary_OC01_ARN0051 [HG-U133_Plus_2]///geo_access
title: Breast metastasis in the ovary_OC01_ARN0053 [HG-U133_Plus_2]///geo_access
title: Breast metastasis in the ovary_OC01_ARN0055 [HG-U133_Plus_2]///geo_access
title: Breast metastasis in the ovary_OC01_ARN0060 [HG-U133_Plus_2]///geo_access
title: Breast metastasis in the ovary_OC01_ARN0069 [HG-U133_Plus_2]///geo_access
title: Breast metastasis in the ovary_OC01_ARN0073 [HG-U133_Plus_2]///geo_access
title: Breast metastasis in the ovary_OC01_ARN0077 [HG-U133_Plus_2]///geo_access
title: Breast metastasis in the ovary_OC01_ARN0079 [HG-U133_Plus_2]///geo_access
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title: Breast metastasis in the ovary_OC01_ARN0099 [HG-U133_Plus_2]///geo_access
title: Breast metastasis in the ovary_OC01_ARN0102 [HG-U133_Plus_2]///geo_access
title: Breast metastasis in the ovary_OC01_ARN0104 [HG-U133_Plus_2]///geo_access
title: Breast metastasis in the ovary_OC01_ARN0112 [HG-U133_Plus_2]///geo_access
title: Breast metastasis in the ovary_OC01_ARN0120 [HG-U133_Plus_2]///geo_access
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title: Breast metastasis in the ovary_OC01_ARN0123 [HG-U133_Plus_2]///geo_access
title: Breast metastasis in the ovary_OC01_ARN0126 [HG-U133_Plus_2]///geo_access
title: Breast metastasis in the ovary_OC01_ARN0141 [HG-U133_Plus_2]///geo_access
title: Breast metastasis in the ovary_OC01_ARN0142 [HG-U133_Plus_2]///geo_access
title: Breast metastasis in the ovary_OC01_ARN0143 [HG-U133_Plus_2]///geo_access
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title: Breast metastasis in the ovary_OC01_ARN0145 [HG-U133_Plus_2]///geo_access

title: Breast metastasis in the ovary_OC01_ARN0146 [HG-U133_Plus_2]///geo_access

title: Breast metastasis in the ovary_OC01_ARN0153 [HG-U133_Plus_2]///geo_access

title: Breast metastasis in the ovary_OC01_ARN0162 [HG-U133_Plus_2]///geo_access

title: Breast metastasis in the ovary_OC01_ARN0201 [HG-U133_Plus_2]///geo_access

title: Ovarian carcinoma_OC0

title: Ovarian carcinoma_OC01_ARN00

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC0

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01

title: Ovarian carcinoma_OC0

title: Ovarian carcinoma_OC0

title: Ovarian carcinoma_OC01_AR

title: Ovarian carcinoma_OC0

title: Ovarian carcinoma_OC0

title: Ovarian carcinoma_OC0

title: Ovarian carcinoma_OC0

title: Ovarian carcinoma_OC0

title: Ovarian carcinoma_OC01_ARN003

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC0

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_ARN00

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_ARN004

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_ARN

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC0

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_ARN0076

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_ARN

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_ARN0091

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_

title: Ovarian carcinoma_OC01_AR

```
                                                   title: Ovarian carcinoma_OC01

                                               title: Ovarian carcinoma_OC01_ARN

                                                  title: Ovarian carcinoma_OC01_

                                                  title: Ovarian carcinoma_OC01_

                                                  title: Ovarian carcinoma_OC01_

                                                  title: Ovarian carcinoma_OC01_

                                                  title: Ovarian carcinoma_OC01_

                                              title: Ovarian carcinoma_OC01_ARN0

                                                  title: Ovarian carcinoma_OC01_

                                             title: Ovarian carcinoma_OC01_ARN01

                                          title: Ovarian carcinoma_OC01_ARN0114

                                              title: Ovarian carcinoma_OC01_ARN0

                                                    title: Ovarian carcinoma_OC0

                                                  title: Ovarian carcinoma_OC01_

                                                  title: Ovarian carcinoma_OC01_

                                                  title: Ovarian carcinoma_OC01_

                                                  title: Ovarian carcinoma_OC01_



duplicates:
GSE20565.GSE20565_GSM516722 GSE20565.GSE20565_GSM516741
                          1                           1
                       NA's
                        138
```

Value

An expression set

`GSE2109` *IGC EXpression Project for Oncology*

Description

EXpression Project for Oncology, International Genomics Consortium, www.intgen.org

Format

```
experimentData(eset):
Experiment data
  Experimenter name: EXpression Project for Oncology, International Genomics Con
  Laboratory: expO, IGC 2005
  Contact information:
  Title: IGC EXpression Project for Oncology
  URL:
  PMIDs: PMID unknown

  Abstract: A 8 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
   platform_shorttitle:
      Affymetrix HG-U133Plus2
   platform_summary:
      hgu133plus2
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL570
   version:
      2015-09-22 19:40:35

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
    (42447 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 42447 features, 204 samples
Platform type:
---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
Abdominal wall mass - 8176             Omentum - 1006
                         1                          1
            Omentum - 8174             Omentum - 8186
```

```
             1                          1
Omentum - 8240             Ovary - 101094
             1                          1
Ovary - 101109             Ovary - 101120
             1                          1
Ovary - 101150               Ovary - 1018
             1                          1
  Ovary - 1040               Ovary - 1057
             1                          1
Ovary - 112866             Ovary - 112867
             1                          1
Ovary - 118662             Ovary - 118671
             1                          1
  Ovary - 1241               Ovary - 1270
             1                          1
Ovary - 129660             Ovary - 129669
             1                          1
  Ovary - 1311               Ovary - 1313
             1                          1
  Ovary - 1323             Ovary - 133643
             1                          1
Ovary - 133651               Ovary - 1351
             1                          1
Ovary - 151614             Ovary - 151622
             1                          1
Ovary - 161465             Ovary - 161524
             1                          1
Ovary - 161525             Ovary - 161534
             1                          1
  Ovary - 1636               Ovary - 1639
             1                          1
  Ovary - 1643             Ovary - 170809
             1                          1
Ovary - 174931             Ovary - 174936
             1                          1
Ovary - 180953             Ovary - 184837
             1                          1
Ovary - 187243             Ovary - 187246
             1                          1
Ovary - 187251             Ovary - 187253
             1                          1
Ovary - 191413             Ovary - 191424
             1                          1
Ovary - 195198             Ovary - 199399
             1                          1
Ovary - 199400             Ovary - 202030
             1                          1
Ovary - 202041              Ovary - 20284
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 Ovary - 20285              Ovary - 20296
             1                          1
 Ovary - 20307              Ovary - 20315
```

```
                       1                          1
           Ovary - 20323              Ovary - 20325
                       1                          1
           Ovary - 20326              Ovary - 20329
                       1                          1
          Ovary - 207532             Ovary - 209699
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          Ovary - 209709             Ovary - 209714
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          Ovary - 209718             Ovary - 211371
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          Ovary - 211409              Ovary - 21758
                       1                          1
          Ovary - 219571             Ovary - 219581
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          Ovary - 219590             Ovary - 219604
                       1                          1
           Ovary - 21981              Ovary - 22218
                       1                          1
          Ovary - 226414             Ovary - 226423
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                       1                          1
          Ovary - 235692             Ovary - 235695
                       1                          1
           Ovary - 23862              Ovary - 23884
                       1                          1
           Ovary - 23904              Ovary - 23930
                       1                          1
           Ovary - 23934              Ovary - 23936
                       1                          1
           Ovary - 23938             Ovary - 241181
                       1                          1
          Ovary - 241187             Ovary - 241196
                       1                          1
          Ovary - 241198             Ovary - 241199
                       1                          1
          Ovary - 242929                    (Other)
                       1                        105

sample_type:
tumor
  204

histological_type:
       clearcell             endo         mucinous             other
```

```
               9                28               11               59
             ser undifferentiated             NA's
              85                2               10

primarysite:
other    ov  NA's
   23   178     3

summarygrade:
high  low NA's
  91   31   82

summarystage:
early  late  NA's
   37    87    80

tumorstage:
   1    2    3    4 NA's
  20   14   58   18   94

substage:
   a    b    c NA's
  17   22   79   86

grade:
   1    2    3    4 NA's
  11   20   83    8   82

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  25.00   45.00   55.00   58.82   65.00   85.00

batch:
2004-12-03 2004-12-04 2004-12-07 2005-02-11 2005-03-03 2005-03-10 2005-03-11
         3          3          1          1          1          1          1
2005-03-15 2005-03-16 2005-03-17 2005-03-19 2005-03-22 2005-04-13 2005-04-26
         3          1          2          4          2          1          5
2005-04-29 2005-05-10 2005-06-01 2005-06-03 2005-06-08 2005-06-17 2005-08-05
         2          2          5          3          3          6          3
2005-08-09 2005-08-11 2005-09-07 2005-09-09 2005-09-13 2005-11-02 2005-11-04
         1          6          1          3          3          6          3
2005-11-15 2005-11-18 2005-12-02 2006-01-24 2006-01-26 2006-02-07 2006-02-28
         3          1          4          2          1          1          1
2006-03-06 2006-03-14 2006-04-18 2006-04-20 2006-05-16 2006-06-08 2006-07-26
         2          2          1          2          3          1          2
2006-07-28 2006-09-12 2006-09-14 2006-10-10 2006-10-24 2006-10-31 2006-11-09
         1          2          1          1          9          5         10
2006-11-21 2006-11-30 2006-12-07 2007-01-12 2007-02-09 2007-03-07 2007-03-09
         1          6          3          1          1          8          1
2007-03-15 2007-05-01 2007-05-03 2007-05-15 2007-05-18 2007-05-30 2007-06-12
         4          2          3          4          2          2          1
2007-07-27 2007-09-05 2007-09-07 2007-09-11 2007-09-12 2008-02-15 2008-02-21
```

```
         2          3          1          4          4          1          3
2008-02-27 2008-03-04 2008-05-13 2008-05-16 2008-05-23
         2          1          4          4          5

uncurated_author_metadata:
```

```
                                                                  title: Omentu
```

```
title: Ovary - 170809///geo_accession: GSM137917///status: Public on Sep 28 2006
```

```
duplicates:
GSE2109.GSE2109_GSM76554 GSE2109.GSE2109_GSM76567                          NA's
```

```
                       1                         1                     202
```

Value

An expression set

GSE26193 *miR-141 and miR-200a act on ovarian tumorigenesis by controlling oxidative stress response.*

Description

Although there is evidence that redox regulation has an essential role in malignancies, its impact on tumor prognosis remains unclear. Here we show crosstalk between oxidative stress and the miR-200 family of microRNAs that affects tumorigenesis and chemosensitivity. miR-141 and miR-200a target p38?? and modulate the oxidative stress response. Enhanced expression of these microRNAs mimics p38?? deficiency and increases tumor growth in mouse models, but it also improves the response to chemotherapeutic agents. High-grade human ovarian adenocarcinomas that accumulate miR-200a have low concentrations of p38?? and an associated oxidative stress signature. The miR200a-dependent stress signature correlates with improved survival of patients in response to treatment. Therefore, the role of miR-200a in stress could be a predictive marker for clinical outcome in ovarian cancer. In addition, although oxidative stress promotes tumor growth, it also sensitizes tumors to treatment, which could account for the limited success of antioxidants in clinical trials.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Mateescu B, Batista L, Mariani O, Meyniel J, Cottu PH, Sast
  Laboratory: Mateescu, Mechta-Grigoriou 2011
  Contact information:
  Title: miR-141 and miR-200a act on ovarian tumorigenesis by controlling oxidat
  URL:
  PMIDs: 22101765

  Abstract: A 149 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
   platform_shorttitle:
      Affymetrix HG-U133Plus2
   platform_summary:
      hgu133plus2
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
```

```
      GPL570
   platform_technology:
      in situ oligonucleotide
   version:
      2015-09-22 19:44:56

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
    (42447 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 42447 features, 107 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

      n  events  median 0.95LCL 0.95UCL
 107.00   76.00    3.05    2.50    4.56

---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
  Ovarian carcinoma 1  Ovarian carcinoma 10 Ovarian carcinoma 100
                    1                    1                     1
Ovarian carcinoma 101 Ovarian carcinoma 102 Ovarian carcinoma 103
                    1                     1                     1
Ovarian carcinoma 104 Ovarian carcinoma 105 Ovarian carcinoma 106
                    1                     1                     1
Ovarian carcinoma 107  Ovarian carcinoma 11  Ovarian carcinoma 12
                    1                     1                     1
 Ovarian carcinoma 13  Ovarian carcinoma 14  Ovarian carcinoma 15
                    1                     1                     1
 Ovarian carcinoma 16  Ovarian carcinoma 17  Ovarian carcinoma 18
                    1                     1                     1
 Ovarian carcinoma 19   Ovarian carcinoma 2  Ovarian carcinoma 20
                    1                     1                     1
 Ovarian carcinoma 21  Ovarian carcinoma 22  Ovarian carcinoma 23
                    1                     1                     1
 Ovarian carcinoma 24  Ovarian carcinoma 25  Ovarian carcinoma 26
                    1                     1                     1
 Ovarian carcinoma 27  Ovarian carcinoma 28  Ovarian carcinoma 29
                    1                     1                     1
  Ovarian carcinoma 3  Ovarian carcinoma 30  Ovarian carcinoma 31
                    1                     1                     1
 Ovarian carcinoma 32  Ovarian carcinoma 33  Ovarian carcinoma 34
                    1                     1                     1
```

```
 Ovarian carcinoma 35  Ovarian carcinoma 36  Ovarian carcinoma 37 
                    1                     1                     1 
 Ovarian carcinoma 38  Ovarian carcinoma 39   Ovarian carcinoma 4 
                    1                     1                     1 
 Ovarian carcinoma 40  Ovarian carcinoma 41  Ovarian carcinoma 42 
                    1                     1                     1 
 Ovarian carcinoma 43  Ovarian carcinoma 44  Ovarian carcinoma 45 
                    1                     1                     1 
 Ovarian carcinoma 46  Ovarian carcinoma 47  Ovarian carcinoma 48 
                    1                     1                     1 
 Ovarian carcinoma 49   Ovarian carcinoma 5  Ovarian carcinoma 50 
                    1                     1                     1 
 Ovarian carcinoma 51  Ovarian carcinoma 52  Ovarian carcinoma 53 
                    1                     1                     1 
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  Ovarian carcinoma 6  Ovarian carcinoma 60  Ovarian carcinoma 61 
                    1                     1                     1 
 Ovarian carcinoma 62  Ovarian carcinoma 63  Ovarian carcinoma 64 
                    1                     1                     1 
 Ovarian carcinoma 65  Ovarian carcinoma 66  Ovarian carcinoma 67 
                    1                     1                     1 
 Ovarian carcinoma 68  Ovarian carcinoma 69   Ovarian carcinoma 7 
                    1                     1                     1 
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                    1                     1                     1 
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                    1                     1                     1 
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                    1                     1                     1 
 Ovarian carcinoma 79   Ovarian carcinoma 8  Ovarian carcinoma 80 
                    1                     1                     1 
 Ovarian carcinoma 81  Ovarian carcinoma 82  Ovarian carcinoma 83 
                    1                     1                     1 
 Ovarian carcinoma 84  Ovarian carcinoma 85  Ovarian carcinoma 86 
                    1                     1                     1 
 Ovarian carcinoma 87  Ovarian carcinoma 88  Ovarian carcinoma 89 
                    1                     1                     1 
  Ovarian carcinoma 9  Ovarian carcinoma 90  Ovarian carcinoma 91 
                    1                     1                     1 
              (Other) 
                    8 
```

```
sample_type:
tumor 
  107 
```

```
histological_type:
clearcell      endo  mucinous     other       ser 
        6         8         8         6        79 
```

```
summarygrade:
high  low
  67   40

summarystage:
early  late
   31    76

tumorstage:
 1  2  3  4
20 11 59 17

substage:
   a    b    c NA's
  16   12   62   17

grade:
 1  2  3
 7 33 67

days_to_tumor_recurrence:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    3.0   340.5   584.0  1108.0  1525.0  7386.0

recurrence_status:
norecurrence   recurrence
          27           80

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
      3     668    1096    1520    2220    7386

vital_status:
deceased   living
      76       31

batch:
2006-06-01 2006-06-27 2006-06-28 2006-06-29 2006-06-30 2006-07-20 2008-03-06
        15         14         23         16         21          3          1
2009-03-18 2009-03-19
         4         10

uncurated_author_metadata:
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            title: Ovarian carcinoma 101///geo_accession: GSM643033///status: Pu

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          title: Ovarian carcinoma 103///geo_accession: GSM643035///status: Publ
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title: Ovarian carcinoma 91///geo_accession: GSM643023///status: Public on
title: Ovarian carcinoma 92///geo_accession: GSM643024///status: Publi
```

Value

An expression set

`GSE26712` *A gene signature predicting for survival in suboptimally debulked patients with ovarian cancer.*

Description

Despite the existence of morphologically indistinguishable disease, patients with advanced ovarian tumors display a broad range of survival end points. We hypothesize that gene expression profiling can identify a prognostic signature accounting for these distinct clinical outcomes. To resolve survival-associated loci, gene expression profiling was completed for an extensive set of 185 (90 optimal/95 suboptimal) primary ovarian tumors using the Affymetrix human U133A microarray. Cox regression analysis identified probe sets associated with survival in optimally and suboptimally debulked tumor sets at a P value of <0.01. Leave-one-out cross-validation was applied to each tumor cohort and confirmed by a permutation test. External validation was conducted by applying the gene signature to a publicly available array database of expression profiles of advanced stage suboptimally debulked tumors. The prognostic signature successfully classified the tumors according to survival for suboptimally (P = 0.0179) but not optimally debulked (P = 0.144) patients. The suboptimal gene signature was validated using the independent set of tumors (odds ratio, 8.75; P = 0.0146). To elucidate signaling events amenable to therapeutic intervention in suboptimally debulked patients, pathway analysis was completed for the top 57 survival-associated probe sets. For suboptimally debulked patients, confirmation of the predictive gene signature supports the existence of a clinically relevant predictor, as well as the possibility of novel therapeutic opportunities. Ultimately, the prognostic classifier defined for suboptimally debulked tumors may aid in the classification and enhancement of patient outcome for this high-risk population.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Bonome T, Levine DA, Shih J, Randonovich M, Pise-Masison CA
  Laboratory: Bonome, Birrer 2008
  Contact information:
  Title: A gene signature predicting for survival in suboptimally debulked patie
  URL:
  PMIDs: 18593951

  Abstract: A 238 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133A] Affymetrix Human Genome U133A Array
   platform_shorttitle:
      Affymetrix HG-U133A
   platform_summary:
      hgu133a
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL96
   version:
      2015-09-22 19:46:24

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
    (20967 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 20967 features, 195 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

   10 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
 185.00  129.00    3.83    3.24    4.83

---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
     Normal HOSE2008      Normal HOSE2061      Normal HOSE2064
                   1                    1                    1
     Normal HOSE2085      Normal HOSE2225      Normal HOSE2226
                   1                    1                    1
     Normal HOSE2228      Normal HOSE2230      Normal HOSE2234
                   1                    1                    1
     Normal HOSE2237  Ovarian Cancer SO10 Ovarian Cancer SO100
                   1                    1                    1
Ovarian Cancer SO103 Ovarian Cancer SO106 Ovarian Cancer SO108
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 Ovarian Cancer SO11 Ovarian Cancer SO113 Ovarian Cancer SO115
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Ovarian Cancer SO116 Ovarian Cancer SO117 Ovarian Cancer SO118
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 Ovarian Cancer SO12 Ovarian Cancer SO121 Ovarian Cancer SO122
                   1                    1                    1
Ovarian Cancer SO124 Ovarian Cancer SO129  Ovarian Cancer SO13
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Ovarian Cancer SO137 Ovarian Cancer SO141 Ovarian Cancer SO143
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Ovarian Cancer SO174  Ovarian Cancer SO18 Ovarian Cancer SO181
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                   1                    1                    1
Ovarian Cancer SO203 Ovarian Cancer SO205  Ovarian Cancer SO21
```

```
                   1                    1                    1
Ovarian Cancer SO211 Ovarian Cancer SO214 Ovarian Cancer SO216
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Ovarian Cancer SO225 Ovarian Cancer SO227 Ovarian Cancer SO228
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Ovarian Cancer SO243 Ovarian Cancer SO244 Ovarian Cancer SO246
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Ovarian Cancer SO247 Ovarian Cancer SO249  Ovarian Cancer SO25
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Ovarian Cancer SO268 Ovarian Cancer SO272 Ovarian Cancer SO273
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Ovarian Cancer SO278 Ovarian Cancer SO279 Ovarian Cancer SO282
                   1                    1                    1
Ovarian Cancer SO283 Ovarian Cancer SO285 Ovarian Cancer SO290
                   1                    1                    1
             (Other)
                  96

sample_type:
healthy   tumor
     10     185

histological_type:
 ser NA's
 185   10

primarysite:
 ov
195

summarygrade:
high NA's
 185   10

summarystage:
late NA's
 185   10
```

```
tumorstage:
   3    4 NA's 
 146   36   13 

substage:
   b    c NA's 
   9  137   49 

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  26.00   52.00   63.00   61.54   70.00   84.00      13 

recurrence_status:
norecurrence   recurrence 
          42          153 

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   21.9   660.6  1164.0  1429.0  1880.0  4982.0      10 

vital_status:
deceased   living     NA's 
     129       56       10 

debulking:
   optimal suboptimal       NA's 
        90         95         10 

percent_normal_cells:
20- 
195 

percent_stromal_cells:
20- 
195 

percent_tumor_cells:
80+ 
195 

batch:
2003-11-04 2003-11-05 2003-11-06 2003-11-07 2003-11-20 2003-11-21 2003-12-16 
        14         16          9          6         10         15         17 
2003-12-23 2003-12-24 2004-04-20 2004-04-21 2004-04-27 2004-09-28 2005-07-27 
        12         11         20         17          9         14         15 
2006-11-09 
        10 

uncurated_author_metadata:
                                                                       title: No

                                                                       title: No
```

title: No

title: No

title: No

title: No

title: No

title: No

title: No

title: No

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title: Ovarian Cancer SO244///geo_accession: GSM657595///status: Public on
title: Ovarian Cancer SO246///geo_accession: GSM657596///status: Public
title: Ovarian Cancer SO247///geo_accession: GSM657597///status: Public on
title: Ovarian Cancer SO249///geo_accession: GSM657598///status: Public on
title: Ovarian Cancer SO250///geo_accession: GSM657600///status: Public on
```

```
     title: Ovarian Cancer SO256///geo_accession: GSM657601///status: Public on
      title: Ovarian Cancer SO257///geo_accession: GSM657602///status: Public on
     title: Ovarian Cancer SO258///geo_accession: GSM657603///status: Public on
           title: Ovarian Cancer SO25///geo_accession: GSM657599///status: Publi
     title: Ovarian Cancer SO261///geo_accession: GSM657604///status: Public on
     title: Ovarian Cancer SO262///geo_accession: GSM657605///status: Public on
     title: Ovarian Cancer SO263///geo_accession: GSM657606///status: Public on
     title: Ovarian Cancer SO265///geo_accession: GSM657607///status: Public on
      title: Ovarian Cancer SO267///geo_accession: GSM657608///status: Public on
        title: Ovarian Cancer SO268///geo_accession: GSM657609///status: Public
     title: Ovarian Cancer SO272///geo_accession: GSM657610///status: Public on
        title: Ovarian Cancer SO273///geo_accession: GSM657611///status: Public
        title: Ovarian Cancer SO278///geo_accession: GSM657612///status: Public
     title: Ovarian Cancer SO279///geo_accession: GSM657613///status: Public on
      title: Ovarian Cancer SO282///geo_accession: GSM657614///status: Public on
     title: Ovarian Cancer SO283///geo_accession: GSM657615///status: Public on
     title: Ovarian Cancer SO285///geo_accession: GSM657616///status: Public on
         title: Ovarian Cancer SO290///geo_accession: GSM657617///status: Public
     title: Ovarian Cancer SO295///geo_accession: GSM657618///status: Public on


duplicates:
                              GSE26712.GSE26712_GSM657526
                                                        1
GSE26712.GSE26712_GSM657526///GSE26712.GSE26712_GSM657527
                                                        1
                              GSE26712.GSE26712_GSM657527
                                                        1
                                                     NA's
                                                      192
```

Value

An expression set

GSE30009 *Multidrug resistance-linked gene signature predicts overall survival of patients with primary ovarian serous carcinoma.*

Description

This study assesses the ability of multidrug resistance (MDR)-associated gene expression patterns to predict survival in patients with newly diagnosed carcinoma of the ovary. The scope of this research differs substantially from that of previous reports, as a very large set of genes was evaluated whose expression has been shown to affect response to chemotherapy.We applied a customized TaqMan low density array, a highly sensitive and specific assay, to study the expression profiles of 380 MDR-linked genes in 80 tumor specimens collected at initial surgery to debulk primary serous carcinoma. The RNA expression profiles of these drug resistance genes were correlated with clinical outcomes.Leave-one-out cross-validation was used to estimate the ability of MDR gene expression to predict survival. Although gene expression alone does not predict overall survival (OS; P = 0.06), four covariates (age, stage, CA125 level, and surgical debulking) do (P = 0.03). When gene expression was added to the covariates, we found an 11-gene signature that provides a major improvement in OS prediction (log-rank statistic P < 0.003). The predictive power of this 11-gene signature was confirmed by dividing high- and low-risk patient groups, as defined by their clinical covariates, into four specific risk groups on the basis of expression levels.This study reveals an 11-gene signature that allows a more precise prognosis for patients with serous cancer of the ovary treated with carboplatin- and paclitaxel-based therapy. These 11 new targets offer opportunities for new therapies to improve clinical outcome in ovarian cancer.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Gillet JP, Calcagno AM, Varma S, Davidson B et al. Multidru
  Laboratory: Gillet, Gottesman 2012
  Contact information:
  Title: Multidrug resistance-linked gene signature predicts overall survival of
  URL:
  PMIDs: 22492981

  Abstract: A 244 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      TaqMan qRT-PCR Homo sapiens Low-Density Array 380
   platform_shorttitle:
      TaqMan qRT-PCR
   platform_summary:
      NA
   platform_manufacturer:
      TaqMan
   platform_distribution:
```

```
      custom
   platform_accession:
      GPL13728
   version:
      2015-09-22 19:46:26

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 5 6 ... 380 (363 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 363 features, 103 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

      n  events  median 0.95LCL 0.95UCL
 103.00   57.00    3.42    2.92    5.34

---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
 Norwegian patient 1 Norwegian patient 10 Norwegian patient 11
                   1                    1                    1
Norwegian patient 12 Norwegian patient 13 Norwegian patient 14
                   1                    1                    1
Norwegian patient 15 Norwegian patient 16 Norwegian patient 17
                   1                    1                    1
Norwegian patient 18 Norwegian patient 19  Norwegian patient 2
                   1                    1                    1
Norwegian patient 20 Norwegian patient 21 Norwegian patient 22
                   1                    1                    1
Norwegian patient 23  Norwegian patient 3  Norwegian patient 4
                   1                    1                    1
 Norwegian patient 5  Norwegian patient 6  Norwegian patient 7
                   1                    1                    1
 Norwegian patient 8  Norwegian patient 9         US Patient 1
                   1                    1                    1
       US Patient 10        US Patient 11        US Patient 12
                   1                    1                    1
       US Patient 13        US Patient 14        US Patient 15
                   1                    1                    1
       US Patient 16        US Patient 17        US Patient 18
                   1                    1                    1
       US Patient 19         US Patient 2        US Patient 20
                   1                    1                    1
       US Patient 21        US Patient 22        US Patient 23
```

```
                1                    1                    1
     US Patient 24        US Patient 25        US Patient 26
                1                    1                    1
     US Patient 27        US Patient 28        US Patient 29
                1                    1                    1
      US Patient 3        US Patient 30        US Patient 31
                1                    1                    1
     US Patient 32        US Patient 33        US Patient 34
                1                    1                    1
     US Patient 35        US Patient 36        US Patient 37
                1                    1                    1
     US Patient 38        US Patient 39         US Patient 4
                1                    1                    1
     US Patient 40        US Patient 41        US Patient 42
                1                    1                    1
     US Patient 43        US Patient 44        US Patient 45
                1                    1                    1
     US Patient 46        US Patient 47        US Patient 48
                1                    1                    1
     US Patient 49         US Patient 5        US Patient 50
                1                    1                    1
     US Patient 51        US Patient 52        US Patient 53
                1                    1                    1
     US Patient 54        US Patient 55        US Patient 56
                1                    1                    1
     US Patient 57        US Patient 58        US Patient 59
                1                    1                    1
      US Patient 6        US Patient 60        US Patient 61
                1                    1                    1
     US Patient 62        US Patient 63        US Patient 64
                1                    1                    1
     US Patient 65        US Patient 66        US Patient 67
                1                    1                    1
     US Patient 68        US Patient 69         US Patient 7
                1                    1                    1
     US Patient 70        US Patient 71        US Patient 72
                1                    1                    1
     US Patient 73        US Patient 74        US Patient 75
                1                    1                    1
     US Patient 76        US Patient 77        US Patient 78
                1                    1                    1
          (Other)
                4

sample_type:
tumor
  103

histological_type:
clearcell       ser
        1       102
```

```
summarygrade:
high  low NA's 
  92    9    2 

summarystage:
late 
 103 

tumorstage:
 3  4 
82 21 

substage:
   b    c NA's 
   2   60   41 

grade:
   1    2    3 NA's 
   4    5   92    2 

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
  30.00   56.00   61.00   62.45   71.50   87.00 

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
     24     598    1053    1156    1568    4748 

vital_status:
deceased   living 
      57       46 

debulking:
   optimal suboptimal 
        81         22 

uncurated_author_metadata:
```

title: US P

title:

title: US Patien

title: US Patient 51///geo_accession: GSM742615///status: Public on Apr 19 2012/

title: US Patient 54///geo_accession: GSM7

title: US Patient 57///geo_accession: GSM742621///status: Publi

title: US Patient 59///geo_accession: GSM742623///status: Publi

title: US Patient 63///geo_acces

title: US Patie

title: US Patient 66///geo_accession: GSM742630///sta

```
title: US Patient 70///geo_accession: GSM742634///status: Public on Apr 19
```

```
title: US Pat
title: US Patient 75///geo_accession: GSM7
titl
title: US Patient 77///ge
title: US Patient 78
title: US Patient 79/
```

Value

An expression set

`GSE30161` *Multi-gene expression predictors of single drug responses to adjuvant chemotherapy in ovarian carcinoma: predicting platinum resistance.*

Description

Despite advances in radical surgery and chemotherapy delivery, ovarian cancer is the most lethal gynecologic malignancy. Standard therapy includes treatment with platinum-based combination chemotherapies yet there is no biomarker model to predict their responses to these agents. We here have developed and independently tested our multi-gene molecular predictors for forecasting patients' responses to individual drugs on a cohort of 55 ovarian cancer patients. To independently validate these molecular predictors, we performed microarray profiling on FFPE tumor samples of 55 ovarian cancer patients (UVA-55) treated with platinum-based adjuvant chemotherapy. Genome-wide chemosensitivity biomarkers were initially discovered from the in vitro drug activities and genomic expression data for carboplatin and paclitaxel, respectively. Multivariate predictors were trained with the cell line data and then evaluated with a historical patient cohort. For the UVA-55 cohort, the carboplatin, taxol, and combination predictors significantly stratified responder patients and non-responder patients (p = 0.019, 0.04, 0.014) with sensitivity = 91%, 96%, 93 and NPV = 57%, 67%, 67% in pathologic clinical response. The combination predictor also demonstrated a significant survival difference between predicted responders and non-responders with a median survival of 55.4 months vs. 32.1 months. Thus, COXEN single- and combination-drug predictors successfully stratified platinum resistance and taxane response in an independent cohort of ovarian cancer patients based on their FFPE tumor samples.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Ferriss JS, Kim Y, Duska L, Birrer M, Levine DA, Moskaluk C
  Laboratory: Ferriss, Lee 2012
  Contact information:
  Title: Multi-gene expression predictors of single drug responses to adjuvant c
  URL:
  PMIDs: 22348014

  Abstract: A 215 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
   platform_shorttitle:
      Affymetrix HG-U133Plus2
   platform_summary:
      hgu133plus2
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL570
   version:
      2015-09-22 19:50:24

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
    (42447 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 42447 features, 58 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

      n  events  median 0.95LCL 0.95UCL
```

```
  58.00   36.00    4.19    2.70    6.17

---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
 OV_FFPE_1 OV_FFPE_10 OV_FFPE_11 OV_FFPE_12 OV_FFPE_13 OV_FFPE_14 OV_FFPE_15
         1          1          1          1          1          1          1
OV_FFPE_16 OV_FFPE_17 OV_FFPE_18 OV_FFPE_19  OV_FFPE_2 OV_FFPE_20 OV_FFPE_21
         1          1          1          1          1          1          1
OV_FFPE_22 OV_FFPE_23 OV_FFPE_24 OV_FFPE_25 OV_FFPE_26 OV_FFPE_27 OV_FFPE_28
         1          1          1          1          1          1          1
OV_FFPE_29  OV_FFPE_3 OV_FFPE_30 OV_FFPE_31 OV_FFPE_32 OV_FFPE_33 OV_FFPE_34
         1          1          1          1          1          1          1
OV_FFPE_35 OV_FFPE_36 OV_FFPE_37 OV_FFPE_38 OV_FFPE_39  OV_FFPE_4 OV_FFPE_40
         1          1          1          1          1          1          1
OV_FFPE_41 OV_FFPE_42 OV_FFPE_43 OV_FFPE_44 OV_FFPE_45 OV_FFPE_46 OV_FFPE_47
         1          1          1          1          1          1          1
OV_FFPE_48 OV_FFPE_49  OV_FFPE_5 OV_FFPE_50 OV_FFPE_51 OV_FFPE_52 OV_FFPE_53
         1          1          1          1          1          1          1
OV_FFPE_54 OV_FFPE_55 OV_FFPE_56 OV_FFPE_57 OV_FFPE_58  OV_FFPE_6  OV_FFPE_7
         1          1          1          1          1          1          1
 OV_FFPE_8  OV_FFPE_9
         1          1

sample_type:
tumor
   58

histological_type:
       clearcell              endo          mucinous             other
               5                 1                 1                 1
             ser undifferentiated              NA's
              47                 1                 2

summarygrade:
high  low NA's
  33   21    4

summarystage:
late
  58

tumorstage:
 3  4
53  5

substage:
 a  b  c
 9 11 38
```

```
grade:
   1    2    3 NA's 
   2   19   33    4 

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
  38.00   53.50   62.00   62.57   72.00   85.00 

pltx:
 y 
58 

tax:
 n  y 
 4 54 

neo:
 n 
58 

days_to_tumor_recurrence:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
   12.0   255.2   386.0   742.1   768.2  4208.0 

recurrence_status:
norecurrence   recurrence         NA's 
           6           48            4 

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
   49.0   585.2  1010.0  1375.0  2131.0  4208.0 

vital_status:
deceased   living 
      36       22 

debulking:
   optimal suboptimal       NA's 
        26         30          2 

batch:
2009-10-07 2009-10-08 2009-10-09 2009-10-20 
        28         18          8          4 

uncurated_author_metadata:
            title: OV_FFPE_10///geo_accession: GSM746870///status: Public on Aug

  title: OV_FFPE_11///geo_accession: GSM746871///status: Public on Aug 21 2012//

    title: OV_FFPE_12///geo_accession: GSM746872///status: Public on Aug 21 2012

    title: OV_FFPE_13///geo_accession: GSM746873///status: Public on Aug 21 2012
```

title: OV_FFPE_14///geo_accession: GSM746874///status: Public on Aug 21 2012/

title: OV_FFPE_15///geo_accession: GSM746875///status:

title: OV_FFPE_16///geo_accession: GSM746876///status: Public on Aug 21 20

title: OV_FFPE_17///geo_accession: GSM746877///status: Public on Aug 21 2

title: OV_FFPE_18///geo_accession: GSM

title: OV_FFPE_19///g

title: OV_FFPE_1///geo_accession: GSM746861///status: Public on Aug 21 20

title: OV_FFPE_20///geo_accession: GSM746880///status: Public on Aug 21 2012//

title: OV_FFPE_21///geo_accession: GSM746881///status: Pub

title: OV_FFPE_22///geo_accession: G

title: OV_FFPE_23///geo_accession: GSM746883///status: Public on Aug 2

title: OV_FFPE_24///geo_accession: GSM746884///status: Public on Aug 21

title: OV_FFPE_25///geo_accession: GSM746885///status: Public on Aug 21 2

title: OV_FFPE_26///geo_accession: GSM746886///status: Public on Aug 21 201

title: OV_FFPE_27///geo_accession: GSM746887///status: Public on Aug 21 2012/

title: OV_FFPE_28///geo_accession: GSM746888///s

title: OV_FFPE_29///geo_accession: GSM746889///status: Public on Aug 21 20

title: OV_FFPE_2///geo_accession: GSM746862///status: Public on Aug 21 201

title: OV_FFPE_30///geo_accession: GSM746890///status: Public on Aug

title: OV_FFPE_31///geo_accession: GSM746891///status: Public on Aug 21 2

title: OV_FFPE_32///geo_accession: GSM746892///status: Public on Aug 21 2012///

title: OV_FFPE_33///geo_accession: GSM746893///status: Public on Aug 21 2012///s

title: OV_FFPE_34///geo_accession: GSM746894///status: Public on Aug 2

title: OV_FFPE_35///geo_accession: GSM746895///status: Public on Aug 21 2012//

title: OV_FFPE_36///geo_accession: GSM746896///status: Public on Aug 21 20

title: OV_FFPE_37///geo_accession: GSM746897//

title: OV_FFPE_38///geo_accession: GSM746898///status: Public on Aug 21 2012///

title: OV_FFPE_39///geo_accession: GSM746899///status: Public on Aug 21 201

title: OV_FFPE_3///geo_accession: GSM746863///status: Public on Aug 21 201

title: OV_FFPE_40///geo_accession: GSM746900///status: Public on Aug 21 201

title: OV_FFPE_41///geo_accession: GS

title: OV_FFPE_42///geo_accession: GSM746902///status: Public on Aug 21 2012//

title: OV_FFPE_43///geo_accession: GSM746903///st

title: OV_FFPE_44///geo_accession: GSM746904///status: Public on Aug 21 2012///

title: OV_FFPE_45///geo_accession: GSM746905///status: Public on Aug 21 2012///

title: OV_FFPE_46///geo_accession: GSM746906///status: Public on Aug 21 201

title: OV_FFPE_47///geo_accession: GSM746907///status: Public on Aug 21 201

title: OV_FFPE_48///geo_accession: GSM746908///status:

title: OV_FFPE_49///geo_accession: GSM746909///status: Public on Aug 21 20

title: OV_FFPE_4///geo_accession: GSM746864///status: Public on Aug 2

title: OV_FFPE_50///geo_accession: GSM746910///status: Public on Aug 21 20

title: OV_FFPE_51///geo_accession: GSM746911///status: Public on Aug 21

title: OV_FFPE_52///geo_accession: GSM746912///status: Public on Aug 21

title: OV_FFPE_53///geo_accession: GSM746913///status: Public on Aug 21 201

title: OV_FFPE_54///geo_accession: GSM746914///status: Public on Aug 21 201

title: OV_FFPE_55///geo_accession: GSM746915///status: Public on Aug 21 20

title: OV_FFPE_56///geo_accession: GSM746916///status: Public on Aug 21 2012//

title: OV_FFPE_57///geo_accession: GS

title: OV_FFPE_58///geo_accession: GSM746918///status: Public on Aug 21 201

title: OV_FFPE_5///geo_accession: GSM746865///status: Public on Aug 21 2

title: OV_FFPE_6///geo_accession: GSM746866///status: Public on Aug 21 2

title: OV_FFPE_7///geo_accession: GSM746867///status: Public on Aug 21 20

```
    title: OV_FFPE_8///geo_accession: GSM746868///status: Public on Aug 21 2
  title: OV_FFPE_9///geo_accession: GSM746869///status: Public on Aug 21 201
```

Value

An expression set

`GSE32062` *High-risk ovarian cancer based on 126-gene expression signature is uniquely characterized by downregulation of antigen presentation pathway.*

Description

High-grade serous ovarian cancers are heterogeneous not only in terms of clinical outcome but also at the molecular level. Our aim was to establish a novel risk classification system based on a gene expression signature for predicting overall survival, leading to suggesting novel therapeutic strategies for high-risk patients.In this large-scale cross-platform study of six microarray data sets consisting of 1,054 ovarian cancer patients, we developed a gene expression signature for predicting overall survival by applying elastic net and 10-fold cross-validation to a Japanese data set A (n = 260) and evaluated the signature in five other data sets. Subsequently, we investigated differences in the biological characteristics between high- and low-risk ovarian cancer groups.An elastic net analysis identified a 126-gene expression signature for predicting overall survival in patients with ovarian cancer using the Japanese data set A (multivariate analysis, P = 4 ?? 10(-20)). We validated its predictive ability with five other data sets using multivariate analysis (Tothill's data set, P = 1 ?? 10(-5); Bonome's data set, P = 0.0033; Dressman's data set, P = 0.0016; TCGA data set, P = 0.0027; Japanese data set B, P = 0.021). Through gene ontology and pathway analyses, we identified a significant reduction in expression of immune-response-related genes, especially on the antigen presentation pathway, in high-risk ovarian cancer patients.This risk classification based on the 126-gene expression signature is an accurate predictor of clinical outcome in patients with advanced stage high-grade serous ovarian cancer and has the potential to develop new therapeutic strategies for high-grade serous ovarian cancer patients.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Yoshihara K, Tsunoda T, Shigemizu D, Fujiwara H et al. High
  Laboratory: Yoshihara, Tanaka 2012
  Contact information:
  Title: High-risk ovarian cancer based on 126-gene expression signature is uniq
  URL:
  PMIDs: 22241791

  Abstract: A 255 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
```

```
   platform_title:
      Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (Probe Name vers
ion)
   platform_shorttitle:
      Agilent G4112F
   platform_summary:
      hgug4112a
   platform_manufacturer:
      Agilent
   platform_distribution:
      commercial
   platform_accession:
      GPL6480
   version:
      2015-09-22 19:55:29

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A_23_P100001 A_23_P100011 ... A_32_P99902 (30936 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 30936 features, 260 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

      n  events  median 0.95LCL 0.95UCL
 260.00  121.00    4.93    4.11    6.58

---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
    10d    115d    116d    117d    119d     11d    120d    122d    123d   125Rd
      1       1       1       1       1       1       1       1       1       1
   129d     12d    130d    132d    134d    139d    140d    143d    144d    145d
      1       1       1       1       1       1       1       1       1       1
   146d    148d    150d    155d    156d     15d    160d     16d    171d    173d
      1       1       1       1       1       1       1       1       1       1
   174d    178d     17d    183d    184d    185d    186d     18d     20d     22d
      1       1       1       1       1       1       1       1       1       1
    23d    249d    257d     25d    260d    262d    264d    266d    267d    268d
      1       1       1       1       1       1       1       1       1       1
   269d     27d    299d      2d    300d    301d    302d    303d    304d   305d2
      1       1       1       1       1       1       1       1       1       1
   306d    307d    310d    318d    319d   320d2    323d    327d    330d    331d
      1       1       1       1       1       1       1       1       1       1
  333d2    335d    337d    340d    342d    346d    347d   348d2    350d    352d
```

```
      1       1       1       1       1       1       1       1       1       1
   353d    355d    356d    357d    358d    360d    362d    363d    365d    366d
      1       1       1       1       1       1       1       1       1       1
   367d   368d2     36d     38d   41d2R     42d     43d     44d    456d (Other)
      1       1       1       1       1       1       1       1       1     161

sample_type:
tumor
  260

histological_type:
ser
260

summarygrade:
high  low
 129  131

summarystage:
late
 260

tumorstage:
  3   4
204  56

substage:
   a    b    c NA's
   4   20  180   56

grade:
  2   3
131 129

pltx:
  y
260

tax:
  y
260

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
     30     810    1245    1344    1710    3840

vital_status:
deceased   living
     121      139

debulking:
   optimal suboptimal
```

```
       103        157

uncurated_author_metadata:
     title: serous ovarian cancer 10d///geo_accession: GSM794865///status: Publi

title: serous ovarian cancer 115d///geo_accession: GSM794867///status: Public on

title: serous ovarian cancer 116d///geo_accession: GSM794868///status: Public on

   title: serous ovarian cancer 117d///geo_accession: GSM794869///status: Public

   title: serous ovarian cancer 119d///geo_accession: GSM794870///status: Public

     title: serous ovarian cancer 11d///geo_accession: GSM794866///status: Publi

   title: serous ovarian cancer 120d///geo_accession: GSM794872///status: Public

 title: serous ovarian cancer 122d///geo_accession: GSM794873///status: Public c

title: serous ovarian cancer 123d///geo_accession: GSM794874///status: Public on

title: serous ovarian cancer 125Rd///geo_accession: GSM794875///status: Public c

   title: serous ovarian cancer 129d///geo_accession: GSM794876///status: Public

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                               NA's
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258
```

Value

An expression set

GSE32063 *High-risk ovarian cancer based on 126-gene expression signature is uniquely characterized by downregulation of antigen presentation pathway.*

Description

High-grade serous ovarian cancers are heterogeneous not only in terms of clinical outcome but also at the molecular level. Our aim was to establish a novel risk classification system based on a gene expression signature for predicting overall survival, leading to suggesting novel therapeutic strategies for high-risk patients.In this large-scale cross-platform study of six microarray data sets consisting of 1,054 ovarian cancer patients, we developed a gene expression signature for predicting overall survival by applying elastic net and 10-fold cross-validation to a Japanese data set A (n = 260) and evaluated the signature in five other data sets. Subsequently, we investigated differences in the biological characteristics between high- and low-risk ovarian cancer groups.An elastic net analysis identified a 126-gene expression signature for predicting overall survival in patients with ovarian cancer using the Japanese data set A (multivariate analysis, P = 4 ?? 10(-20)). We validated its predictive ability with five other data sets using multivariate analysis (Tothill's data set, P = 1 ?? 10(-5); Bonome's data set, P = 0.0033; Dressman's data set, P = 0.0016; TCGA data set, P = 0.0027; Japanese data set B, P = 0.021). Through gene ontology and pathway analyses, we identified a significant reduction in expression of immune-response-related genes, especially on the antigen presentation pathway, in high-risk ovarian cancer patients.This risk classification based on the 126-gene expression signature is an accurate predictor of clinical outcome in patients with advanced stage high-grade serous ovarian cancer and has the potential to develop new therapeutic strategies for high-grade serous ovarian cancer patients.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Yoshihara K, Tsunoda T, Shigemizu D, Fujiwara H et al. High
  Laboratory: Yoshihara, Tanaka 2012
  Contact information:
  Title: High-risk ovarian cancer based on 126-gene expression signature is uniq
  URL:
  PMIDs: 22241791

  Abstract: A 255 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (Probe Name vers
ion)
   platform_shorttitle:
```

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      Agilent G4112F
   platform_summary:
      hgug4112a
   platform_manufacturer:
      Agilent
   platform_distribution:
      commercial
   platform_accession:
      GPL6480
   version:
      2015-09-22 19:58:23

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A_23_P100001 A_23_P100011 ... A_32_P99902 (30936 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 30936 features, 40 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

      n  events  median 0.95LCL 0.95UCL
  40.00   22.00    4.44    3.29      NA

---------------------------
Available sample meta-data:
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alt_sample_name:
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 222  224  226  229  230  231  274  277  278  280  281  282  283  284  285  286
   1    1    1    1    1    1    1    1    1    1    1    1    1    1    1    1
 287  288  289  291  292  294 297R 298R
   1    1    1    1    1    1    1    1

sample_type:
tumor
   40

histological_type:
ser
 40

summarygrade:
high  low
  17   23
```

```
summarystage:
late 
  40 

tumorstage:
 3  4 
31  9 

substage:
   b    c NA's 
   3   28    9 

grade:
 2  3 
23 17 

pltx:
 y 
40 

tax:
 y 
40 

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
    210     705    1155    1346    1792    3330 

vital_status:
deceased   living 
      22       18 

debulking:
   optimal suboptimal 
        19         21 

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title: serous ovarian cancer 229///geo_accession:

title: serous ovarian cancer 230///geo_accessio

title: serous ovarian cancer 231///geo_accession:

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title: serous ovarian cancer 288///geo_accession: G

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title: serous ovarian cancer 291///geo_accession: GSM7
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    title: serous ovarian cancer 294///geo_accession: G
 title: serous ovarian cancer 297R///geo_accession: GS
title: serous ovarian cancer 298R///geo_accession: GSM
```

Value

An expression set

`GSE44104` *COL11A1 promotes tumor progression and predicts poor clinical outcome in ovarian cancer.*

Description

Biomarkers that predict disease progression might assist the development of better therapeutic strategies for aggressive cancers, such as ovarian cancer. Here, we investigated the role of collagen type XI alpha 1 (COL11A1) in cell invasiveness and tumor formation and the prognostic impact of COL11A1 expression in ovarian cancer. Microarray analysis suggested that COL11A1 is a disease progression-associated gene that is linked to ovarian cancer recurrence and poor survival. Small interference RNA-mediated specific reduction in COL11A1 protein levels suppressed the invasive ability and oncogenic potential of ovarian cancer cells and decreased tumor formation and lung colonization in mouse xenografts. A combination of experimental approaches, including real-time RT-PCR, casein zymography and chromatin immunoprecipitation (ChIP) assays, showed that COL11A1 knockdown attenuated MMP3 expression and suppressed binding of Ets-1 to its putative MMP3 promoter-binding site, suggesting that the Ets-1-MMP3 axis is upregulated by COL11A1. Transforming growth factor (TGF)-beta (TGF-??1) treatment triggers the activation of smad2 signaling cascades, leading to activation of COL11A1 and MMP3. Pharmacological inhibition of MMP3 abrogated the TGF-??1-triggered, COL11A1-dependent cell invasiveness. Furthermore, the NF-YA-binding site on the COL11A1 promoter was identified as the major determinant of TGF-??1-dependent COL11A1 activation. Analysis of 88 ovarian cancer patients indicated that high COL11A1 mRNA levels are associated with advanced disease stage. The 5-year recurrence-free and overall survival rates were significantly lower (P=0.006 and P=0.018, respectively) among patients with high expression levels of tissue COL11A1 mRNA compared with those with low expression. We conclude that COL11A1 may promote tumor aggressiveness via the TGF-??1-MMP3 axis and that COL11A1 expression can predict clinical outcome in ovarian cancer patients.

Format

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experimentData(eset):
Experiment data
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  Experimenter name: Wu Y, Chang T, Huang Y, Huang H, Chou C
  Laboratory: Wu, Chou 2013
  Contact information:
  Title: COL11A1 promotes tumor progression and predicts poor clinical outcome i
  URL:
  PMIDs: 23934190

  Abstract: A 260 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
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      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
   platform_shorttitle:
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      hgu133plus2
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      Affymetrix
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      commercial
   platform_accession:
      GPL570
   platform_technology:
      in situ oligonucleotide
   version:
      2015-09-22 20:02:05

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
    (42447 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
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Details

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assayData: 42447 features, 60 samples
Platform type:
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Available sample meta-data:
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 Tc_94  Te_69  Te_77  Te_78  Te_79  Te_84  Te_87  Te_89  Te_90  Te_91  Te_92
     1      1      1      1      1      1      1      1      1      1      1
 Te_93 Tm_101 Tm_102 Tm_106 Tm_107 Tm_110  Tm_95  Tm_96  Tm_97  Tm_98  Ts_11
     1      1      1      1      1      1      1      1      1      1      1
 Ts_14  Ts_15  Ts_17  Ts_19   Ts_2  Ts_20  Ts_21  Ts_23  Ts_24  Ts_26  Ts_28
     1      1      1      1      1      1      1      1      1      1      1
  Ts_3  Ts_31  Ts_32  Ts_34  Ts_35  Ts_36  Ts_37  Ts_39   Ts_4  Ts_41  Ts_43
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 Ts_45  Ts_46  Ts_47   Ts_5   Ts_8
     1      1      1      1      1

sample_type:
tumor
   60

histological_type:
clearcell      endo  mucinous       ser
       12        11         9        28

summarystage:
early  late
   25    35

tumorstage:
 1  2  3  4
17  8 30  5

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os_binary:
 long short
   44    16

relapse_binary:
 long short
   40    20

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title: Ts_5///geo_accession: GSM1079030///status: Public on Ja
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duplicates:
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Value

An expression set

GSE49997 *Validating the impact of a molecular subtype in ovarian cancer on outcomes: a study of the OVCAD Consortium.*

Description

Most patients with epithelial ovarian cancer (EOC) are diagnosed at advanced stage and have a poor prognosis. However, a small proportion of these patients will survive, whereas others will die very quickly. Clinicopathological factors do not allow precise identification of these subgroups. Thus, we have validated a molecular subclassification as new prognostic factor in EOC. One hundred and ninety-four patients with Stage II-IV EOC were characterized by whole-genome expression profiling of tumor tissues and were classified using a published 112 gene set, derived from an International Federation of Gynecology and Obstetrics (FIGO) stage-directed supervised classification approach. The 194 tumor samples were classified into two subclasses comprising 95 (Subclass 1) and 99 (Subclass 2) tumors. All nine FIGO II tumors were grouped in Subclass 1 (P = 0.001). Subclass 2 (54% of advanced-stage tumors) was significantly correlated with peritoneal carcinomatosis and non-optimal debulking. Patients with Subclass 2 tumors had a worse overall survival for both serous and non-serous histological subtypes, as revealed by univariate analysis (hazard ratios [HR] of 3.17 and 17.11, respectively; P ??? 0.001) and in models corrected for relevant clinicopathologic parameters (HR 2.87 and 12.42, respectively; P ??? 0.023). Significance analysis of microarrays revealed 2082 genes that were differentially expressed in advanced-grade serous tumors of both subclasses and the focal adhesion pathway as the most deregulated pathway. In the present validation study, we have shown that, in advanced-stage serous ovarian cancer, two approximately equally large molecular subtypes exist, independent of classical clinocopathological parameters and presenting with highly different whole-genome expression profiles and a markedly different overall survival. Similar results were obtained in a small cohort of patients with non-serous tumors.?? 2012 Japanese Cancer Association.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Pils D1, Hager G, Tong D, Aust S, Heinze G, Kohl M, Schuste
  Laboratory: Pils, Zeilinger 2012 
  Contact information:  
  Title: Validating the impact of a molecular subtype in ovarian cancer on outco
  URL:  
  PMIDs: 22497737 

  Abstract: A 276 word abstract is available. Use 'abstract' method.
```

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    notes:
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        ABI Human Genome Survey Microarray Version 2
     platform_shorttitle:
        ABI Human Genome
     platform_summary:

     platform_manufacturer:
        Applied Biosystems
     platform_distribution:
        commercial
     platform_accession:
        GPL2986
     platform_technology:
        in situ oligonucleotide
     version:
        2015-09-22 20:04:13

  featureData(eset):
  An object of class 'AnnotatedDataFrame'
    featureNames: 100027 100036 ... 10715781 (18439 total)
    varLabels: probeset gene EntrezGene.ID best_probe
    varMetadata: labelDescription
```

Details

```
assayData: 18439 features, 204 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

   10 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
 194.00   57.00      NA    3.67      NA

---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
EOC P001 EOC P002 EOC P003 EOC P004 EOC P005 EOC P006 EOC P007 EOC P008
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EOC P009 EOC P010 EOC P011 EOC P012 EOC P013 EOC P014 EOC P015 EOC P016
       1        1        1        1        1        1        1        1
EOC P017 EOC P018 EOC P019 EOC P020 EOC P021 EOC P022 EOC P023 EOC P024
       1        1        1        1        1        1        1        1
EOC P025 EOC P026 EOC P027 EOC P028 EOC P029 EOC P030 EOC P031 EOC P032
       1        1        1        1        1        1        1        1
EOC P033 EOC P034 EOC P035 EOC P036 EOC P037 EOC P038 EOC P039 EOC P040
       1        1        1        1        1        1        1        1
EOC P041 EOC P042 EOC P043 EOC P044 EOC P045 EOC P046 EOC P047 EOC P048
```

```
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EOC P049 EOC P050 EOC P051 EOC P052 EOC P053 EOC P054 EOC P055 EOC P056
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EOC P057 EOC P058 EOC P059 EOC P060 EOC P061 EOC P062 EOC P063 EOC P064
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EOC P065 EOC P066 EOC P067 EOC P068 EOC P069 EOC P070 EOC P071 EOC P072
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EOC P073 EOC P074 EOC P075 EOC P076 EOC P077 EOC P078 EOC P079 EOC P080
       1        1        1        1        1        1        1        1
EOC P081 EOC P082 EOC P083 EOC P084 EOC P085 EOC P086 EOC P087 EOC P088
       1        1        1        1        1        1        1        1
EOC P089 EOC P090 EOC P091 EOC P092 EOC P093 EOC P094 EOC P095 EOC P096
       1        1        1        1        1        1        1        1
EOC P097 EOC P098 EOC P099  (Other) 
       1        1        1      105 

sample_type:
tumor 
  204 

histological_type:
other   ser  NA's 
   23   171    10 

summarygrade:
high  low NA's 
 143   50   11 

summarystage:
early  late  NA's 
    9   185    10 

tumorstage:
   2    3    4 NA's 
   9  154   31   10 

grade:
   2    3 NA's 
  50  143   11 

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  26.00   50.00   57.00   57.66   67.00   85.00      10 

days_to_tumor_recurrence:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   30.0   335.0   487.0   580.1   722.5  1461.0      10 

recurrence_status:
norecurrence   recurrence         NA's 
          70          124           10 
```

```
days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   30.0   517.0   745.5   782.9  1027.0  1491.0      10 

vital_status:
deceased   living     NA's 
      57      137       10 

debulking:
   optimal suboptimal       NA's 
       137         57         10 

uncurated_author_metadata:
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Value

An expression set

`GSE51088` *POSTN/TGFBI-associated stromal signature predicts poor prognosis in serous epithelial ovarian cancer.*

Description

To identify molecular prognosticators and therapeutic targets for high-grade serous epithelial ovarian cancers (EOCs) using genetic analyses driven by biologic features of EOC pathogenesis.Ovarian tissue samples (n = 172; 122 serous EOCs, 30 other EOCs, 20 normal/benign) collected prospectively from sequential patients undergoing gynecologic surgery were analyzed using RNA expression microarrays. Samples were classified based on expression of genes with potential relevance in ovarian cancer. Gene sets were defined using Rosetta Similarity Search Tool (ROAST) and analysis of variance (ANOVA). Gene copy number variations were identified by array comparative genomic hybridization.No distinct subgroups of EOC could be identified by unsupervised clustering, however, analyses based on genes correlated with periostin (POSTN) and estrogen receptor-alpha (ESR1) yielded distinct subgroups. When 95 high-grade serous EOCs were grouped by genes based on ANOVA comparing ESR1/WT1 and POSTN/TGFBI samples, overall survival (OS) was significantly shorter for 43 patients with tumors expressing genes associated with POSTN/TGFBI compared to 52 patients with tumors expressing genes associated with ESR1/WT1 (median 30 versus 49 months, respectively; P = 0.022). Several targets with therapeutic potential were identified within each subgroup. BRCA germline mutations were more frequent in the ESR1/WT1 subgroup. Proliferation-associated genes and TP53 status (mutated or wild-type) did not correlate with survival. Findings were validated using independent ovarian cancer datasets.Two distinct molecular subgroups of high-grade serous EOCs based on POSTN/TGFBI and ESR1/WT1 expressions were identified with significantly different OS. Specific differentially expressed genes between these subgroups provide potential prognostic and therapeutic targets.Copyright ?? 2013 Elsevier Inc. All rights reserved.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Karlan BY, Dering J, Walsh C, Orsulic S, Lester J, Anderson
  Laboratory: Karlan, Slamon 2014
  Contact information:
  Title: POSTN/TGFBI-associated stromal signature predicts poor prognosis in ser
  URL:
  PMIDs: 24368280

  Abstract: A 250 word abstract is available. Use 'abstract' method.
```

```
    Information is available on: preprocessing
    notes:
     platform_title:
        Agilent-012097 Human 1A Microarray (V2) G4110B (Probe Name version)
     platform_shorttitle:
        Agilent G4110B
     platform_summary:
        hgug4110b
     platform_manufacturer:
        Agilent
     platform_distribution:
        commercial
     platform_accession:
        GPL7264
     platform_technology:
        in situ oligonucleotide
     version:
        2015-09-22 20:05:48

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A_23_P100001 A_23_P100011 ... A_23_P99996 (18703 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 18703 features, 172 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

   20 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
 152.00  112.00    4.13    3.50    4.92

---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
Ov_Tumor_Ref_Mix vs. CS-OV-001 Ov_Tumor_Ref_Mix vs. CS-OV-002
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Ov_Tumor_Ref_Mix vs. CS-OV-003 Ov_Tumor_Ref_Mix vs. CS-OV-004
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Ov_Tumor_Ref_Mix vs. CS-OV-007 Ov_Tumor_Ref_Mix vs. CS-OV-008
                             1                              1
Ov_Tumor_Ref_Mix vs. CS-OV-009 Ov_Tumor_Ref_Mix vs. CS-OV-010
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Ov_Tumor_Ref_Mix vs. CS-OV-011 Ov_Tumor_Ref_Mix vs. CS-OV-012
```

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Ov_Tumor_Ref_Mix vs. CS-OV-013 Ov_Tumor_Ref_Mix vs. CS-OV-014
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Ov_Tumor_Ref_Mix vs. CS-OV-015 Ov_Tumor_Ref_Mix vs. CS-OV-016
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Ov_Tumor_Ref_Mix vs. CS-OV-017 Ov_Tumor_Ref_Mix vs. CS-OV-018
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Ov_Tumor_Ref_Mix vs. CS-OV-019 Ov_Tumor_Ref_Mix vs. CS-OV-020
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Ov_Tumor_Ref_Mix vs. CS-OV-021 Ov_Tumor_Ref_Mix vs. CS-OV-022
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Ov_Tumor_Ref_Mix vs. CS-OV-029 Ov_Tumor_Ref_Mix vs. CS-OV-030
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Ov_Tumor_Ref_Mix vs. CS-OV-031 Ov_Tumor_Ref_Mix vs. CS-OV-032
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Ov_Tumor_Ref_Mix vs. CS-OV-033 Ov_Tumor_Ref_Mix vs. CS-OV-034
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Ov_Tumor_Ref_Mix vs. CS-OV-035 Ov_Tumor_Ref_Mix vs. CS-OV-036
                             1                              1
Ov_Tumor_Ref_Mix vs. CS-OV-037 Ov_Tumor_Ref_Mix vs. CS-OV-038
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Ov_Tumor_Ref_Mix vs. CS-OV-039 Ov_Tumor_Ref_Mix vs. CS-OV-040
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Ov_Tumor_Ref_Mix vs. CS-OV-045 Ov_Tumor_Ref_Mix vs. CS-OV-046
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```

```
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Ov_Tumor_Ref_Mix vs. CS-OV-095 Ov_Tumor_Ref_Mix vs. CS-OV-096
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Ov_Tumor_Ref_Mix vs. CS-OV-097 Ov_Tumor_Ref_Mix vs. CS-OV-098
                            1                              1
Ov_Tumor_Ref_Mix vs. CS-OV-099                       (Other)
                            1                             73

sample_type:
    benign borderline    healthy metastatic      tumor
         5         12         15         17        123

histological_type:
clearcell      endo  mucinous     other       ser      NA's
        3         7         9        11       122        20

summarygrade:
high  low NA's
 119   30   23

summarystage:
early  late  NA's
```

```
   31  120   21

tumorstage:
   1    2    3    4 NA's
  22    9  103   17   21

substage:
   a    b    c NA's
  17   22   94   39

grade:
   0    1    2    3 NA's
   8    8   14  119   23

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   26.0    49.0    57.5    58.6    68.0    91.0

neo:
  n
172

recurrence_status:
norecurrence   recurrence         NA's
          36          111           25

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
     30     791    1491    1835    2344    7001      20

vital_status:
deceased   living     NA's
     112       40       20

percent_normal_cells:
 30- NA's
 140   32

percent_stromal_cells:
 30- NA's
 140   32

percent_tumor_cells:
 70+ NA's
 140   32

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Value

An expression set

`GSE6008` *Lysophosphatidic acid-induced transcriptional profile represents serous epithelial ovarian carcinoma and worsened prognosis.*

Description

Lysophosphatidic acid (LPA) governs a number of physiologic and pathophysiological processes. Malignant ascites fluid is rich in LPA, and LPA receptors are aberrantly expressed by ovarian cancer cells, implicating LPA in the initiation and progression of ovarian cancer. However, there is an absence of systematic data critically analyzing the transcriptional changes induced by LPA in ovarian cancer.In this study, gene expression profiling was used to examine LPA-mediated transcription by exogenously adding LPA to human epithelial ovarian cancer cells for 24 h to mimic long-term stimulation in the tumor microenvironment. The resultant transcriptional profile comprised a 39-gene signature that closely correlated to serous epithelial ovarian carcinoma. Hierarchical clustering of ovarian cancer patient specimens demonstrated that the signature is associated with worsened prognosis. Patients with LPA-signature-positive ovarian tumors have reduced disease-specific and progression-free survival times. They have a higher frequency of stage IIIc serous carcinoma and a greater proportion is deceased. Among the 39-gene signature, a group of seven genes associated with cell adhesion recapitulated the results. Out of those seven, claudin-1, an adhesion molecule and phenotypic epithelial marker, is the only independent biomarker of serous epithelial ovarian carcinoma. Knockdown of claudin-1 expression in ovarian cancer cells reduces LPA-mediated cellular adhesion, enhances suspended cells and reduces LPA-mediated migration.The data suggest that transcriptional events mediated by LPA in the tumor microenvironment influence tumor progression through modulation of cell adhesion molecules like claudin-1 and, for the first time, report an LPA-mediated expression signature in ovarian cancer that predicts a worse prognosis.

Format

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Experiment data
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  Laboratory: Murph, Mills 2009
  Contact information:
  Title: Lysophosphatidic acid-induced transcriptional profile represents serous
  URL:
  PMIDs: 19440550

  Abstract: A 247 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
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   platform_distribution:
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   platform_accession:
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   version:
      2015-09-22 20:07:11

featureData(eset):
An object of class 'AnnotatedDataFrame'
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  varMetadata: labelDescription
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Details

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Available sample meta-data:
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histological_type:
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primarysite:
 ov
103

summarygrade:
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summarystage:
early  late  NA's
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tumorstage:
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  35   11   44    9    4

substage:
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  19   17   38   29

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                      title: Ovarian_Tumor_Serous_KU-OS-013///geo_accession: GSM1394

                      title: Ovarian_Tumor_Serous_KU-OS-015///geo_accession: GSM1394

                      title: Ovarian_Tumor_Serous_KU-OS-018///geo_accession: GSM1394

                      title: Ovarian_Tumor_Serous_KU-OS-021///geo_accession: GSM1394

                      title: Ovarian_Tumor_Serous_KU-OS-022///geo_accession: GSM1394

                        title: Ovarian_Tumor_Serous_UM-OS-02///geo_accession: GSM139

                          title: Ovarian_Tumor_Serous_UM-OS-07///geo_accession: GSM1

                          title: Ovarian_Tumor_Serous_UM-OS-09///geo_accession: GSM1

                           title: Ovarian_Tumor_Serous_UM-OS-10///geo_accession: GSM

                          title: Ovarian_Tumor_Serous_UM-OS-11///geo_accession: GSM1
```

```
duplicates:
GSE6008.GSE6008_GSM139476///GSE6008.GSE6008_GSM139477
                                                    1
GSE6008.GSE6008_GSM139476///GSE6008.GSE6008_GSM139478
                                                    1
GSE6008.GSE6008_GSM139477///GSE6008.GSE6008_GSM139478
                                                    1
```

```
                                                        NA's
                                                         100
```

Value

An expression set

`GSE6822` *Classification of ovarian tumor samples*

Description

Ouellet V, Provencher DM, Maugard CM, Le Page C, Ren F, Lussier C, Novak J, Ge B, Hudson TJ, Tonin PN, Mes-Masson A-M: Discrimination between serous low malignant potential and invasive epithelial ovarian tumors using molecular profiling. Oncogene 2005, 24:4672-4687.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Ouellet V, Provencher DM, Maugard CM, Le Page C, Ren F, Lus
  Laboratory: Ouellet, Mes-Masson 2005
  Contact information:
  Title: Classification of ovarian tumor samples
  URL:
  PMIDs: PMID unknown

  Abstract: A 40 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [Hu6800] Affymetrix Human Full Length HuGeneFL Array
   platform_shorttitle:
      Affymetrix Hu6800
   platform_summary:
      hu6800
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL80
   version:
      2015-09-22 20:07:22

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: A28102_at AB000114_at ... Z97074_at (6407 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 6407 features, 66 samples
Platform type: 
---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
Ovarian tumor AM053 Ovarian tumor AM122 Ovarian tumor AM124 Ovarian tumor AM125 
                  1                   1                   1                   1 
Ovarian tumor AM127 Ovarian tumor AM137 Ovarian tumor AM138 Ovarian tumor AM144 
                  1                   1                   1                   1 
Ovarian tumor AM178 Ovarian tumor AM179 Ovarian tumor AM182 Ovarian tumor AM195 
                  1                   1                   1                   1 
Ovarian tumor AM196 Ovarian tumor AM198 Ovarian tumor AM200 Ovarian tumor AM201 
                  1                   1                   1                   1 
Ovarian tumor AM202 Ovarian tumor AM203 Ovarian tumor AM204 Ovarian tumor AM207 
                  1                   1                   1                   1 
Ovarian tumor AM208 Ovarian tumor AM209 Ovarian tumor AM225 Ovarian tumor AM226 
                  1                   1                   1                   1 
Ovarian tumor AM228 Ovarian tumor AM233 Ovarian tumor AM250 Ovarian tumor AM252 
                  1                   1                   1                   1 
Ovarian tumor AM253 Ovarian tumor AM255 Ovarian tumor AM256 Ovarian tumor AM259 
                  1                   1                   1                   1 
Ovarian tumor AM261 Ovarian tumor AM263 Ovarian tumor AM268 Ovarian tumor AM269 
                  1                   1                   1                   1 
Ovarian tumor AM287 Ovarian tumor AM288 Ovarian tumor AM289 Ovarian tumor AM290 
                  1                   1                   1                   1 
Ovarian tumor AM292 Ovarian tumor AM293 Ovarian tumor AM294 Ovarian tumor AM311 
                  1                   1                   1                   1 
Ovarian tumor AM313 Ovarian tumor AM315 Ovarian tumor AM317 Ovarian tumor AM333 
                  1                   1                   1                   1 
Ovarian tumor AM335 Ovarian tumor AM339 Ovarian tumor AM341 Ovarian tumor AM344 
                  1                   1                   1                   1 
Ovarian tumor AM345 Ovarian tumor AM347 Ovarian tumor AM348 Ovarian tumor AM349 
                  1                   1                   1                   1 
Ovarian tumor AM354 Ovarian tumor AM364 Ovarian tumor AM367 Ovarian tumor AM368 
                  1                   1                   1                   1 
Ovarian tumor AM381 Ovarian tumor AM382 Ovarian tumor AM398 Ovarian tumor AM429 
                  1                   1                   1                   1 
Ovarian tumor AM431 Ovarian tumor AM438 
                  1                   1 

sample_type:
tumor 
   66 

histological_type:
       clearcell             endo              mix         mucinous 
              11                7                3                1 
             ser undifferentiated 
              41                3 
```

```
primarysite:
ov
66

summarygrade:
high  low NA's
  40   15   11

grade:
   1    2    3 NA's
   1   14   40   11

batch:
2000-12-21 2001-05-03 2001-05-29 2001-06-12 2001-09-25 2001-09-26 2001-09-27
         1          1          3          3          1          5          8
2002-02-14 2002-04-17 2002-04-18 2002-07-18 2002-07-24 2002-10-20 2002-10-30
         4          1          9          7          4         10          5
2002-11-01 2002-11-13
         2          2

uncurated_author_metadata:
                                       title: Ovarian tumor AM053///geo_accessio

title: Ovarian tumor AM122///geo_accession: GSM157231///status: Public on Dec 31

                                       title: Ovarian tumor AM124///geo_accessio

                                       title: Ovarian tumor AM125///geo_accessio

             title: Ovarian tumor AM127///geo_accession: GSM157234///status: Pub

                              title: Ovarian tumor AM137///geo_accession: GSM157

                              title: Ovarian tumor AM138///geo_accession: GSM157

                                 title: Ovarian tumor AM144///geo_accession: GSM

                                       title: Ovarian tumor AM178///geo_accessio

                              title: Ovarian tumor AM179///geo_accession: GSM157

                                 title: Ovarian tumor AM182///geo_accession: GSM

                                       title: Ovarian tumor AM195///geo_accessio

                              title: Ovarian tumor AM196///geo_accession: GSM157

                                   title: Ovarian tumor AM198///geo_accession: G

                                 title: Ovarian tumor AM200///geo_accession: GSM
```

title: Ovarian tumor AM201///geo_accession: G

title: Ovarian tumor AM202///geo_accession: G

title: Ovarian tumor AM203///geo_accession: GSM

title: Ovarian tumor AM204///geo_accession: G

title: Ovarian tumor AM207///geo_accession: G

title: Ovarian tumor AM208///geo_accession: G

title: Ovarian tumor AM209///geo_accession: G

title: Ovarian tumor AM225///geo_accession: GS

title: Ovarian tumor AM226///geo_accession: GS

title: Ovarian tumor AM228///geo_accession: GS

title: Ovarian tumor AM233///geo_accession: GS

title: Ovarian tumor AM250///geo_accessi

title: Ovarian tumor AM252///geo_accession: GSM

title: Ovarian tumor AM253///geo_accession: GSM157

title: Ovarian tumor AM255///geo_accessio

title: Ovarian tumor AM256///geo_accessio

title: Ovarian tumor AM259///geo_accession: GSM15

title: Ovarian tumor AM261///geo_accessio

title: Ovarian tumor AM263///geo_accessio

title: Ovarian tumor AM268///geo_accessio

title: Ovarian tumor AM269///geo_accessio

title: Ovarian tumor AM287///geo_accession: GSM157269///status: Publ

title: Ovarian tumor AM288///geo_accession: GSM157270///status: Publ

title: Ovarian tumor AM289///geo_accessio

title: Ovarian tumor AM290///geo_accessio

title: Ovarian tumor AM292///geo_accession: GSM157273///status: Publ title: Ovarian tumor AM293///geo_accessio

title: Ovarian tumor AM294///geo_accessio

title: Ovarian tumor AM311///geo_accession: GSM

title: Ovarian tumor AM313///geo_accession:

title: Ovarian tumor AM315///geo_accession:

title: Ovarian tumor AM317///geo_accession: G

title: Ovarian tumor AM333///geo_accession: G

title: Ovarian tumor AM335///geo_accessio

title: Ovarian tumor AM339///geo_accessio

title: Ovarian tumor AM341///geo_accession

title: Ovarian tumor AM344///geo_accession: GS

title: Ovarian tumor AM345///geo_accessio

title: Ovarian tumor AM347///geo_accession: GSM157286///status: Pub

title: Ovarian tumor AM348///geo_accessio

title: Ovarian tumor AM349///geo_accessio

title: Ovarian tumor AM354///geo_accession: G

title: Ovarian tumor AM364///geo_accession: GSM15729

title: Ovarian tumor AM367///geo_accessio

title: Ovarian tumor AM368///geo_accessio

title: Ovarian tumor AM381///geo_accessio

title: Ovarian tumor AM382///geo_accessio

title: Ovarian tumor AM398///geo_accession: GSM157295///status: Public on Dec

title: Ovarian tumor AM429///geo_accession: GSM157296///status: Public on De

title: Ovarian tumor AM431///geo_accessio

title: Ovarian tumor AM438///geo_accessi

duplicates:

```
   Length     Class      Mode 
       66 character character 
```

Value

An expression set

GSE8842 *Analysis of gene expression in early-stage ovarian cancer.*

Description

Gene expression profile was analyzed in 68 stage I and 15 borderline ovarian cancers to determine if different clinical features of stage I ovarian cancer such as histotype, grade, and survival are related to differential gene expression.Tumors were obtained directly at surgery and immediately frozen in liquid nitrogen until analysis. Glass arrays containing 16,000 genes were used in a dual-color assay labeling protocol.Unsupervised analysis identified eight major patient partitions, one of which was statistically associated to overall survival, grading, and histotype and another with grading and histotype. Supervised analysis allowed detection of gene profiles clearly associated to histotype or to degree of differentiation. No difference was found between borderline and grade 1 tumors. As to recurrence, a subset of genes able to differentiate relapsers from nonrelapsers was identified. Among these, cyclin E and minichromosome maintenance protein 5 were found particularly relevant, as their expression was inversely correlated to progression-free survival (P = 0.00033 and 0.017, respectively).Specific molecular signatures define different histotypes and prognosis of stage I ovarian cancer. Mucinous and clear cells histotypes can be distinguished from the others regardless of tumor grade. Cyclin E and minichromosome maintenance protein 5, whose expression was found previously to be related to a bad prognosis of advanced ovarian cancer, appear to be potential prognostic markers in stage I ovarian cancer too, independent of other pathologic and clinical variables.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Marchini S, Mariani P, Chiorino G, Marrazzo E, Bonomi R, Fr
  Laboratory: Marchini, D'Incalci 2008 
  Contact information:  
  Title: Analysis of gene expression in early-stage ovarian cancer. 
  URL:  
  PMIDs: 19047114 

  Abstract: A 225 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing 
  notes:
   platform_title:     
      Agilent Human 1 cDNA Microarray (G4100A)
   platform_shorttitle:     
      Agilent  G4100A cDNA
   platform_summary:     
      hgug4100a
```

```
    platform_manufacturer:
       Agilent
    platform_distribution:
       custom-commerical
    platform_accession:
       GPL5689
    platform_technology:
       spotted DNA/cDNA
    version:
       2015-09-22 20:07:40

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1 2 ... 8864 (7809 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 7809 features, 83 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

      n  events  median 0.95LCL 0.95UCL
     83      15      NA      12      NA

---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
p0102bis sample_Ovarian tumor p0103bis sample_Ovarian tumor
                            1                             1
p0112bis sample_Ovarian tumor p0114bis sample_Ovarian tumor
                            1                             1
p0125bis sample_Ovarian tumor p0128bis sample_Ovarian tumor
                            1                             1
p0143bis sample_Ovarian tumor p0146bis sample_Ovarian tumor
                            1                             1
p0188bis sample_Ovarian tumor p0208bis sample_Ovarian tumor
                            1                             1
p0210bis sample_Ovarian tumor p0217bis sample_Ovarian tumor
                            1                             1
 p057bis sample_Ovarian tumor  p070bis sample_Ovarian tumor
                            1                             1
 p080bis sample_Ovarian tumor  p091bis sample_Ovarian tumor
                            1                             1
 p139bis sample_Ovarian tumor   p13bis sample_Ovarian tumor
                            1                             1
 p141bis sample_Ovarian tumor  p166bis sample_Ovarian tumor
                            1                             1
```

```
p171bis sample_Ovarian tumor   p17bis sample_Ovarian tumor
                           1                             1
p183bis sample_Ovarian tumor  p209bis sample_Ovarian tumor
                           1                             1
p212bis sample_Ovarian tumor  p213bis sample_Ovarian tumor
                           1                             1
p243bis sample_Ovarian tumor  p246bis sample_Ovarian tumor
                           1                             1
p261bis sample_Ovarian tumor  p284bis sample_Ovarian tumor
                           1                             1
p293bis sample_Ovarian tumor  p310bis sample_Ovarian tumor
                           1                             1
 p31bis sample_Ovarian tumor  p320bis sample_Ovarian tumor
                           1                             1
p331bis sample_Ovarian tumor  p336bis sample_Ovarian tumor
                           1                             1
p350bis sample_Ovarian tumor  p375bis sample_Ovarian tumor
                           1                             1
p382bis sample_Ovarian tumor  p383bis sample_Ovarian tumor
                           1                             1
p386bis sample_Ovarian tumor  p388bis sample_Ovarian tumor
                           1                             1
p398bis sample_Ovarian tumor   p39bis sample_Ovarian tumor
                           1                             1
p401bis sample_Ovarian tumor  p414bis sample_Ovarian tumor
                           1                             1
p421bis sample_Ovarian tumor  p429bis sample_Ovarian tumor
                           1                             1
p433bis sample_Ovarian tumor  p448bis sample_Ovarian tumor
                           1                             1
p455bis sample_Ovarian tumor  p459bis sample_Ovarian tumor
                           1                             1
p462bis sample_Ovarian tumor  p482bis sample_Ovarian tumor
                           1                             1
p487bis sample_Ovarian tumor  p497bis sample_Ovarian tumor
                           1                             1
p502bis sample_Ovarian tumor  p540bis sample_Ovarian tumor
                           1                             1
p541bis sample_Ovarian tumor  p549bis sample_Ovarian tumor
                           1                             1
p550bis sample_Ovarian tumor  p567bis sample_Ovarian tumor
                           1                             1
 p56bis sample_Ovarian tumor  p573bis sample_Ovarian tumor
                           1                             1
p586bis sample_Ovarian tumor  p597bis sample_Ovarian tumor
                           1                             1
p616bis sample_Ovarian tumor   p63bis sample_Ovarian tumor
                           1                             1
p646bis sample_Ovarian tumor   p66bis sample_Ovarian tumor
                           1                             1
 p68bis sample_Ovarian tumor  p690bis sample_Ovarian tumor
                           1                             1
```

```
 p692bis sample_Ovarian tumor  p725bis sample_Ovarian tumor
                            1                             1
  p73bis sample_Ovarian tumor  p760bis sample_Ovarian tumor
                            1                             1
 p770bis sample_Ovarian tumor  p772bis sample_Ovarian tumor
                            1                             1
 p775bis sample_Ovarian tumor  p793bis sample_Ovarian tumor
                            1                             1
  p79bis sample_Ovarian tumor   p84bis sample_Ovarian tumor
                            1                             1
  p90bis sample_Ovarian tumor
                            1

sample_type:
borderline      tumor
        15         68

histological_type:
       clearcell             endo         mucinous            other
              16               17               17                1
             ser undifferentiated
              31                1

primarysite:
ov
83

summarygrade:
high  low NA's
  35   33   15

summarystage:
early
   83

tumorstage:
 1
83

substage:
 a  b  c
25  5 53

grade:
   1    2    3 NA's
  13   20   35   15

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  21.00   43.00   50.00   51.25   61.00   87.00

recurrence_status:
```

```
norecurrence   recurrence
          62           21

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
      0    1192    2248    2273    3048    5824

vital_status:
deceased   living
      15       68

uncurated_author_metadata:
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  title: p0103bis sample_Ovarian tumor///geo_accession: GSM214078///status: Publ

              title: p0112bis sample_Ovarian tumor///geo_accession: GSM214040///

                       title: p0114bis sample_Ovarian tumor///geo_accession: GSM

          title: p0125bis sample_Ovarian tumor///geo_accession: GSM214009///stat

                title: p0128bis sample_Ovarian tumor///geo_accession: GSM214030/

          title: p0143bis sample_Ovarian tumor///geo_accession: GSM214012///stat

          title: p0146bis sample_Ovarian tumor///geo_accession: GSM214033///stat

                 title: p0188bis sample_Ovarian tumor///geo_accession: GSM214041

           title: p0208bis sample_Ovarian tumor///geo_accession: GSM214011///sta

         title: p0210bis sample_Ovarian tumor///geo_accession: GSM214031///statu

              title: p0217bis sample_Ovarian tumor///geo_accession: GSM214008///

      title: p057bis sample_Ovarian tumor///geo_accession: GSM214064///status: P

            title: p070bis sample_Ovarian tumor///geo_accession: GSM214032///sta

         title: p080bis sample_Ovarian tumor///geo_accession: GSM214017///status

          title: p091bis sample_Ovarian tumor///geo_accession: GSM214024///statu

            title: p139bis sample_Ovarian tumor///geo_accession: GSM214047///sta

            title: p13bis sample_Ovarian tumor///geo_accession: GSM214043///stat

   title: p141bis sample_Ovarian tumor///geo_accession: GSM214081///status: Publ

     title: p166bis sample_Ovarian tumor///geo_accession: GSM214013///status: Pu
```

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title: p17bis sample_Ovarian tumor///geo_accession: GSM214080///status: Public

title: p183bis sample_Ovarian tumor///geo_accession: GSM214015///stat

title: p209bis sample_Ovarian tumor///geo_accession: GSM214090///status: Public

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title: p243bis sample_Ovarian tumor///geo_accession: GSM214042///status

title: p246bis sample_Ovarian tumor///geo_accession: GSM214055///status: Pu

title: p261bis sample_Ovarian tumor///geo_accession: GSM214034///stat

title: p284bis sample_Ovarian tumor///geo_accession: GS

title: p293bis sample_Ovarian tumor///geo_accession: GSM214035///status: Pu

title: p310bis sample_Ovarian tumor///geo_accession: GSM214083///status: Public

title: p31bis sample_Ovarian tumor///geo_accession: GSM214019///status

title: p320bis sample_Ovarian tumor///geo_accession: GSM214020///statu

title: p331bis sample_Ovarian tumor///geo_accession: GSM214021///status: P

title: p336bis sample_Ovarian tumor///geo_accession: GSM214056///stat

title: p350bis sample_Ovarian tumor///geo_accession: GSM214036///status: Pu

title: p375bis sample_Ovarian tumor///geo_accession: GSM214048///status: Pu

title: p382bis sample_Ovarian tumor///geo_accession: GSM214037///stat

title: p383bis sample_Ovarian tumor///geo_accession: GSM214029///stat

title: p386bis sample_Ovarian tumor///geo_accession: GSM214038///stat

title: p388bis sample_Ovarian tumor///geo_accession: GSM214059///stat

title: p398bis sample_Ovarian tumor///geo_accession: GSM214066///statu

title: p39bis sample_Ovarian tumor///geo_accession: GSM214076///status: Public

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title: p414bis sample_Ovarian tumor///geo_accession: GSM214051///status: Pu title: p421bis sample_Ovarian tumor///geo_accession: GSM214023///sta

title: p429bis sample_Ovarian tumor///geo_accession: GSM214067///

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title: p502bis sample_Ovarian tumor///geo_accession: GSM214070///status:

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title: p66bis sample_Ovarian tumor///geo_accession: GSM214045///status: Pu

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title: p690bis sample_Ovarian tumor///geo_accession: GSM214072///stat

```
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title: p725bis sample_Ovarian tumor///geo_accession: GSM214057///status:
title: p73bis sample_Ovarian tumor///geo_accession: GSM214028///status: Pu
title: p760bis sample_Ovarian tumor///geo_accession: GSM214062///st
title: p770bis sample_Ovarian tumor///geo_accession: GSM214089///status
title: p772bis sample_Ovarian tumor///geo_accession: GSM214058///status:
title: p775bis sample_Ovarian tumor///geo_accession: GSM214074///status:
title: p793bis sample_Ovarian tumor///geo_accession: GSM214075///status:
title: p79bis sample_Ovarian tumor///geo_accession: GSM214063///status: Pu
title: p84bis sample_Ovarian tumor///geo_accession: GSM214039///status: P
title: p90bis sample_Ovarian tumor///geo_accession: GSM214077///status: Public
```

Value

An expression set

`GSE9891` *Novel molecular subtypes of serous and endometrioid ovarian cancer linked to clinical outcome.*

Description

The study aim to identify novel molecular subtypes of ovarian cancer by gene expression profiling with linkage to clinical and pathologic features.Microarray gene expression profiling was done on 285 serous and endometrioid tumors of the ovary, peritoneum, and fallopian tube. K-means clustering was applied to identify robust molecular subtypes. Statistical analysis identified differentially expressed genes, pathways, and gene ontologies. Laser capture microdissection, pathology review, and immunohistochemistry validated the array-based findings. Patient survival within k-means groups was evaluated using Cox proportional hazards models. Class prediction validated k-means groups in an independent dataset. A semisupervised survival analysis of the array data was used to compare against unsupervised clustering results.Optimal clustering of array data identified six molecular subtypes. Two subtypes represented predominantly serous low malignant potential and low-grade endometrioid subtypes, respectively. The remaining four subtypes represented higher grade and advanced stage cancers of serous and endometrioid morphology. A novel subtype of high-grade serous cancers reflected a mesenchymal cell type, characterized by overexpression of N-cadherin and P-cadherin and low expression of differentiation markers, including CA125 and MUC1. A poor prognosis subtype was defined by a reactive stroma gene expression signature, correlating with extensive desmoplasia in such samples. A similar poor prognosis signature could be found using a semisupervised analysis. Each subtype displayed distinct levels and patterns of immune cell infiltration. Class prediction identified similar subtypes in an independent ovarian dataset with similar prognostic trends.Gene expression profiling identified molecular subtypes of ovarian cancer of biological and clinical importance.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Tothill RW, Tinker AV, George J, Brown R, Fox SB, Lade S, J
  Laboratory: Tothill, Bowtell 2008
  Contact information:
  Title: Novel molecular subtypes of serous and endometrioid ovarian cancer link
  URL:
  PMIDs: 18698038

  Abstract: A 243 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array
   platform_shorttitle:
      Affymetrix HG-U133Plus2
   platform_summary:
      hgu133plus2
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL570
   version:
      2015-09-22 20:16:32

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
    (42447 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 42447 features, 285 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

   7 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
 278.00  113.00    3.95    3.53    5.01
```

```
---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
   X129    X146    X152  X20019  X20025  X20027  X20031  X20032  X20041  X20046
      1       1       1       1       1       1       1       1       1       1
 X20074  X22002  X22012  X22013  X22020  X22023  X22027  X22029  X22031  X22037
      1       1       1       1       1       1       1       1       1       1
 X22046  X22047  X22048  X22057  X22058   X2219   X2227  X23026  X23030  X23036
      1       1       1       1       1       1       1       1       1       1
 X23043  X23052  X23053  X23055  X23066  X23070  X23074  X23077  X23084  X23098
      1       1       1       1       1       1       1       1       1       1
 X23102  X23106  X23116  X23128  X23139  X23143  X23162  X23165  X23167  X23170
      1       1       1       1       1       1       1       1       1       1
 X23172  X23177  X23178  X23182  X23187  X23197  X23202  X23204  X23210  X23212
      1       1       1       1       1       1       1       1       1       1
 X23213  X23221  X26047    X261  X27006  X27098  X32013  X32022  X32032  X32034
      1       1       1       1       1       1       1       1       1       1
 X32048  X32049  X32054  X32055  X32089  X32098  X32103  X32117  X34019  X34049
      1       1       1       1       1       1       1       1       1       1
 X34066  X34078  X34080  X34085  X34086  X34090  X34102  X34103  X34111  X34113
      1       1       1       1       1       1       1       1       1       1
 X34117  X34125  X34165  X34168  X34172  X34186  X34202  X34207  X34801 (Other)
      1       1       1       1       1       1       1       1       1     186

sample_type:
tumor
  285

histological_type:
 endo other   ser
   20     1   264

primarysite:
   ft other    ov
    8    34   243

arrayedsite:
   ft other    ov
    2    83   200

summarygrade:
high  low NA's
 163  116    6

summarystage:
early  late  NA's
   42   240     3

tumorstage:
   1    2    3    4 NA's
```

```
  24   18  218   22    3

substage:
   a    b    c NA's 
  26   19  212   28 

grade:
   1    2    3 NA's 
  19   97  163    6 

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  22.00   53.00   59.00   59.62   68.00   80.00       3 

pltx:
   n    y NA's 
  39  243    3 

tax:
   n    y NA's 
  87  195    3 

neo:
   n    y NA's 
 264   18    3 

days_to_tumor_recurrence:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
    0.0   300.0   450.0   618.9   810.0  4980.0      10 

recurrence_status:
norecurrence   recurrence         NA's 
          94          188            3 

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
    0.0   547.5   855.0   955.1  1252.0  6420.0       7 

vital_status:
deceased   living     NA's 
     113      169        3 

debulking:
   optimal suboptimal       NA's 
       160         88         37 

batch:
2004-12-03 2004-12-23 2005-01-12 2005-01-17 2005-01-24 2005-01-31 2005-02-21 
         3          4          7          7          8         10         10 
2005-03-17 2005-05-05 2005-05-09 2005-05-25 2005-05-27 2005-05-30 2005-06-02 
         2          1          1          2          3          3          6 
2005-06-06 2005-06-08 2005-06-16 2005-06-17 2005-06-24 2005-07-06 2005-07-15 
```

```
         4          5          3          5          6          2          9
2005-07-20 2005-07-29 2005-08-03 2005-08-05 2005-08-18 2005-08-24 2005-08-26
         7          5          6          3          4          8          4
2005-09-09 2005-09-14 2005-09-16 2005-09-21 2005-10-05 2005-10-26 2005-10-28
         4          6          6          4          5          2          4
2005-11-04 2005-11-09 2005-11-11 2005-11-23 2005-12-15 2005-12-21 2006-01-20
         6          3          7          4          7          8          3
2006-01-31 2006-02-08 2006-02-28 2006-04-05 2006-04-06 2006-04-12 2006-04-13
         7          3          3          7          3          7          4
2006-04-28 2006-05-03 2006-06-06 2006-06-07 2006-06-22 2006-07-07 2006-07-19
         6          9          6          3          9          4          7
```

```
uncurated_author_metadata:
               title: X129///geo_accession: GSM250001///status: Public on Mar 01

           title: X146///geo_accession: GSM250000///status: Public on Mar 01 200

     title: X152///geo_accession: GSM249999///status: Public on Mar 01 2008///su

           title: X20019///geo_accession: GSM249998///status: Public on Mar 01 2

    title: X20025///geo_accession: GSM249997///status: Public on Mar 01 2008///s

           title: X20027///geo_accession: GSM249996///status: Public on Mar 01 2

                title: X20031///geo_accession: GSM249995///status: Public on Mar

             title: X20032///geo_accession: GSM249994///status: Public on Mar 01

           title: X20041///geo_accession: GSM249993///status: Public on Mar 01 2

        title: X20046///geo_accession: GSM249992///status: Public on Mar 01 2008

     title: X20074///geo_accession: GSM249991///status: Public on Mar 01 2008///

              title: X22002///geo_accession: GSM249728///status: Public on Mar 0

          title: X22012///geo_accession: GSM249990///status: Public on Mar 01 20

    title: X22013///geo_accession: GSM249989///status: Public on Mar 01 2008///s

           title: X22020///geo_accession: GSM249988///status: Public on Mar 01 2

         title: X22023///geo_accession: GSM249987///status: Public on Mar 01 200

                title: X22027///geo_accession: GSM249725///status: Public on Mar

            title: X22029///geo_accession: GSM249986///status: Public on Mar 01

              title: X22031///geo_accession: GSM249985///status: Public on Mar 0

          title: X22037///geo_accession: GSM249984///status: Public on Mar 01 20
```

```
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title: X22047///geo_accession: GSM249982///status: Public on Mar 01 2008//
title: X22048///geo_accession: GSM249981///status: Public on Mar 01 20
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title: X2227///geo_accession: GSM249977///status: Public on
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title: X23052///geo_accession: GSM249721///status: Public on M
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title: X23102///geo_accession: GSM249966///status: Public on Mar 0
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title: X23116///geo_accession: GSM249964///status: Public on Mar 01 2008//
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title: X32049///geo_accession: GSM249935///status: Public on Mar 01 2008//

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title: X32089///geo_accession: GSM249932///status: Public on Mar 01 2008///subm
title: X32098///geo_accession: GSM249931///status: Public on Mar 01 2008/
title: X32103///geo_accession: GSM249930///status: Public on Mar 01 200
title: X32117///geo_accession: GSM249715///status: Public on M
title: X34019///geo_accession: GSM249929///status: Public on Mar 01 20
title: X34049///geo_accession: GSM249928///status: Public on Mar 01
title: X34066///geo_accession: GSM249927///status: Public on Mar 01 200
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title: X34080///geo_accession: GSM249925///status: Public on Mar 01 20
title: X34085///geo_accession: GSM249924///status: Public on Mar 01 2008
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title: X34090///geo_accession: GSM249922///status: Public on Ma
title: X34102///geo_accession: GSM249921///status: Public on Mar 01 2008///
title: X34103///geo_accession: GSM249920///status: Public on Mar 01 20
title: X34111///geo_accession: GSM249919///status: Public on Mar 01 200
title: X34113///geo_accession: GSM249918///status: Public on Mar 01 2008
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title: X34207///geo_accession: GSM249910///status: Public on Mar 01 2008
```

```
          title: X34801///geo_accession: GSM249909///status: Public on Mar 01 200
```

Value

An expression set

---

loadOvarianDatasets

Function to load ovarian cancer SummarizedExperiment objects from the Experiment Hub

---

Description

This function returns ovarian cancer datasets from the hub and a vector of patients from the datasets that are duplicates based on a spearman correlation > 0.98

Usage

```
loadOvarianDatasets(
  rescale = FALSE,
  minNumberGenes = 0,
  minNumberEvents = 0,
  minSampleSize = 0,
  keepCommonOnly = FALSE,
  imputeMissing = FALSE,
  removeDuplicates = FALSE
)
```

Arguments

`rescale`	apply centering and scaling to the expression sets (default FALSE)
`minNumberGenes`	an integer specifying to remove expression sets with less genes than this number (default 0)
`minNumberEvents`	an integer specifying how man survival events must be in the dataset to keep the dataset (default 0)
`minSampleSize`	an integer specifying the minimum number of patients required in a summarizedExperiment (default 0)
`keepCommonOnly`	remove entrezIDs not common to all datasets (default FALSE)
`imputeMissing`	remove patients from datasets with missing expression values
`removeDuplicates`	remove patients with a Spearman correlation greater than or equal to 0.98 with other patient expression profiles (default TRUE)

Value

a list with 2 elements. The First element named summarizedExperiments contains the datasets. The second element named duplicates contains a vector with patient IDs for the duplicate patients (those with Spearman correlation greater than or equal to 0.98 with other patient expression profiles).

Examples

```
experimentsAndDups = loadOvarianDatasets()
```

`loadOvarianEsets` *Function to load ovarian cancer expression sets from the Experiment Hub*

Description

This function returns ovarian cancer datasets from the hub and a vector of patients from the datasets that are most likely duplicates

Usage

```
loadOvarianEsets(
  removeDuplicates = TRUE,
  quantileCutoff = 0,
  rescale = FALSE,
  minNumberGenes = 0,
  minNumberEvents = 0,
  minSampleSize = 0,
  removeRetracted = TRUE,
  removeSubsets = TRUE,
  keepCommonOnly = FALSE,
  imputeMissing = FALSE
)
```

Arguments

`removeDuplicates`	remove patients with a Spearman correlation greater than or equal to 0.98 with other patient expression profiles (default TRUE)
`quantileCutoff`	A nueric between 0 and 1 specifying to remove genes with standard deviation below the required quantile (default 0)
`rescale`	apply centering and scaling to the expression sets (default FALSE)
`minNumberGenes`	an integer specifying to remove expression sets with less genes than this number (default 0)
`minNumberEvents`	an integer specifying how man survival events must be in the dataset to keep the dataset (default 0)

`minSampleSize`	an integer specifying the minimum number of patients required in an eset (default 0)
`removeRetracted`	remove datasets from retracted papers (default TRUE, currently just PMID17290060 dataset)
`removeSubsets`	remove datasets that are a subset of other datasets (defeault TRUE, currently just PMID19318476)
`keepCommonOnly`	remove probes not common to all datasets (default FALSE)
`imputeMissing`	remove patients from datasets with missing expression values

Value

a list with 2 elements. The First element named esets contains the datasets. The second element named duplicates contains a vector with patient IDs for the duplicate patients (those with Spearman correlation greater than or equal to 0.98 with other patient expression profiles).

Examples

```
esetsAndDups = loadOvarianEsets()
```

`PMID15897565` *Patterns of gene expression that characterize long-term survival in advanced stage serous ovarian cancers.*

Description

A better understanding of the underlying biology of invasive serous ovarian cancer is critical for the development of early detection strategies and new therapeutics. The objective of this study was to define gene expression patterns associated with favorable survival.RNA from 65 serous ovarian cancers was analyzed using Affymetrix U133A microarrays. This included 54 stage III/IV cases (30 short-term survivors who lived <3 years and 24 long-term survivors who lived >7 years) and 11 stage I/II cases. Genes were screened on the basis of their level of and variability in expression, leaving 7,821 for use in developing a predictive model for survival. A composite predictive model was developed that combines Bayesian classification tree and multivariate discriminant models. Leave-one-out cross-validation was used to select and evaluate models.Patterns of genes were identified that distinguish short-term and long-term ovarian cancer survivors. The expression model developed for advanced stage disease classified all 11 early-stage ovarian cancers as long-term survivors. The MAL gene, which has been shown to confer resistance to cancer therapy, was most highly overexpressed in short-term survivors (3-fold compared with long-term survivors, and 29-fold compared with early-stage cases). These results suggest that gene expression patterns underlie differences in outcome, and an examination of the genes that provide this discrimination reveals that many are implicated in processes that define the malignant phenotype.Differences in survival of advanced ovarian cancers are reflected by distinct patterns of gene expression. This biological distinction is further emphasized by the finding that early-stage cancers share expression patterns with the advanced stage long-term survivors, suggesting a shared favorable biology.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Berchuck A, Iversen ES, Lancaster JM, Pittman J, Luo J, Lee
  Laboratory: Berchuck, Marks 2005
  Contact information:
  Title: Patterns of gene expression that characterize long-term survival in adv
  URL:
  PMIDs: 15897565

  Abstract: A 258 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133A] Affymetrix Human Genome U133A Array
   platform_shorttitle:
      Affymetrix HG-U133A
   platform_summary:
      hgu133a
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL96
   warnings:
      These samples are a subset of PMID17290060.
   version:
      2015-09-22 20:17:53

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
    (20967 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 20967 features, 63 samples
Platform type:
---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   1761    1828    1907    2001    2032    2536

sample_type:
tumor
```

```
   63

histological_type:
ser
 63

primarysite:
ov
63

summarygrade:
high  low NA's
  25   37    1

summarystage:
early  late
   11    52

tumorstage:
 1  2  3  4
 7  4 48  4

grade:
   1    2    3    4 NA's
   2   35   24    1    1

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  33.00   52.50   59.00   59.21   67.00   79.00

os_binary:
 long short  NA's
   24    28    11

debulking:
   optimal suboptimal       NA's
        24         28         11

batch:
2002-09-20 2002-10-23 2002-11-12 2002-12-16 2002-12-21 2003-01-03 2003-05-30
        15          9         10          1          3         11         13
2003-07-02
         1

uncurated_author_metadata:
 Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1761///Cancer.Type: Early

 Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1762///Cancer.Type: Early

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1763///Cancer.Type: Early

 Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1764///Cancer.Type: Early
```

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1765///Cancer.Type: Early

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1772///Cancer.Type:

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1773///Cancer.Type:

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1774///Cancer.Type:

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Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1776///Cancer.Type:

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1777///Cancer.Type:

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Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1829///Cancer.Type: S

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1830///Cancer.Type: S

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Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1832///Cancer.Type: S

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1833///Cancer.Type: S

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Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1836///Cancer.Type: S

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1900///Cancer.Type:

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1901///Cancer.Type:

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1902///Cancer.Type:

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1903///Cancer.Type: Early

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1904///Cancer.Type:

Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1905///Cancer.Type: S

```
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1906///Cancer.Type: S
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1907///Cancer.Type:
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1908///Cancer.Type: S
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1909///Cancer.Type: S
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 1989///Cancer.Type:
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2003///Cancer.Type: S
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2004///Cancer.Type: S
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2005///Cancer.Type: S
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2019///Cancer.Type:
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2020///Cancer.Type:
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2021///Cancer.Type:
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2026///Cancer.Type: S
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2027///Cancer.Type: S
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Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2029///Cancer.Type: S
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Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2031///Cancer.Type:
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2032///Cancer.Type:
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2033///Cancer.Type:
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2390///Cancer.Type: Early
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2391///Cancer.Type: Early
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2392///Cancer.Type: Early
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2393///Cancer.Type: Early
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2394///Cancer.Type:
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2395///Cancer.Type:
Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2396///Cancer.Type: S
```

```
        Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2397///Cancer.Type: S
          Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2398///Cancer.Type:
        Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2399///Cancer.Type: S
        Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2400///Cancer.Type: S
        Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2401///Cancer.Type: S
          Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2402///Cancer.Type:
    Genome.ID..File.name....0074_GenomeID_h133a_2802.cel: 2536///Cancer.Type: Early
```

Value

An expression set

`PMID17290060` *An integrated genomic-based approach to individualized treatment of patients with advanced-stage ovarian cancer.*

Description

The purpose of this study was to develop an integrated genomic-based approach to personalized treatment of patients with advanced-stage ovarian cancer. We have used gene expression profiles to identify patients likely to be resistant to primary platinum-based chemotherapy and also to identify alternate targeted therapeutic options for patients with de novo platinum-resistant disease.A gene expression model that predicts response to platinum-based therapy was developed using a training set of 83 advanced-stage serous ovarian cancers and tested on a 36-sample external validation set. In parallel, expression signatures that define the status of oncogenic signaling pathways were evaluated in 119 primary ovarian cancers and 12 ovarian cancer cell lines. In an effort to increase chemotherapy sensitivity, pathways shown to be activated in platinum-resistant cancers were subject to targeted therapy in ovarian cancer cell lines.Gene expression profiles identified patients with ovarian cancer likely to be resistant to primary platinum-based chemotherapy with greater than 80% accuracy. In patients with platinum-resistant disease, we identified expression signatures consistent with activation of Src and Rb/E2F pathways, components of which were successfully targeted to increase response in ovarian cancer cell lines.We have defined a strategy for treatment of patients with advanced-stage ovarian cancer that uses therapeutic stratification based on predictions of response to chemotherapy, coupled with prediction of oncogenic pathway deregulation, as a method to direct the use of targeted agents.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Dressman HK, Berchuck A, Chan G, Zhai J, Bild A, Sayer R, C
  Laboratory: Dressman, Lancaster 2007
```

```
  Contact information:
  Title: An integrated genomic-based approach to individualized treatment of pat
  URL:
  PMIDs: 17290060

  Abstract: A 223 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133A] Affymetrix Human Genome U133A Array
   platform_shorttitle:
      Affymetrix HG-U133A
   platform_summary:
      hgu133a
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL96
   warnings:
      This paper has been retracted.
   version:
      2015-09-22 20:19:16

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
    (20967 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 20967 features, 117 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

      n  events  median 0.95LCL 0.95UCL
 117.00   67.00    5.26    2.79    7.48

---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
   1024    1447    1451    1504    1526    1552    1578    1590    1615    1623
      1       1       1       1       1       1       1       1       1       1
   1665    1674    1675    1774    1784    1834    1846    1877    1913    1929
      1       1       1       1       1       1       1       1       1       1
   2046    2063    2064    2075    2198    2204    2324    2419    2422    2424
```

```
      1       1       1       1       1       1       1       1       1       1
   2465    2476    2479    2505    2542    2573    2673    2739    2802    2849
      1       1       1       1       1       1       1       1       1       1
   2895    2967    2981    2999    3018    3090    3102    3107    3142     860
      1       1       1       1       1       1       1       1       1       1
    872     922   D1805   D1837   D1859   D2098   D2208   D2332   D2342   D2358
      1       1       1       1       1       1       1       1       1       1
  D2421   D2432   D2433   D2480   D2557   D2559   D2560   D2572   D2575   D2576
      1       1       1       1       1       1       1       1       1       1
  D2581   D2603   D2611   D2629   D2640   D2648   D2668   D2689   D2691   D2700
      1       1       1       1       1       1       1       1       1       1
  D2726   D2727   D2733   D2738   D2749   D2776   D2792   M1054   M1055    M120
      1       1       1       1       1       1       1       1       1       1
  M1241   M1390   M1503   M1572     M17   M1891   M2070   M2097   M2184 (Other)
      1       1       1       1       1       1       1       1       1      18

sample_type:
tumor
  117

histological_type:
ser
117

primarysite:
 ov
117

summarygrade:
high  low NA's
  57   57    3

summarystage:
early  late  NA's
    1   115     1

tumorstage:
   2    3    4 NA's
   1   98   17    1

grade:
   1    2    3    4 NA's
   4   53   56    1    3

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
     30     510    1020    1496    2220    5550

vital_status:
deceased   living
      67       50
```

```
primary_therapy_outcome_success:
  completeresponse progressivedisease 
                85                 32 

debulking:
   optimal suboptimal 
        63         54 

batch:
2002-09-20 2002-10-23 2002-11-12 2002-12-16 2002-12-21 2003-01-03 2003-05-30 
        10          8          9          1          3         11         10 
2004-03-09 2004-03-16 2004-04-20 2004-05-18 2004-05-21 2004-05-27 2004-06-22 
        16          6          5         15          7          7          1 
2004-06-23 
         8 

uncurated_author_metadata:
                        OVC.TumorID: 1024///Survival: 13///X0...alive...1...dead

                       OVC.TumorID: 1447///Survival: 75///X0...alive...1...dead:

                       OVC.TumorID: 1451///Survival: 132///X0...alive...1...dead

                        OVC.TumorID: 1504///Survival: 108///X0...alive...1...dea

                       OVC.TumorID: 1526///Survival: 74///X0...alive...1...dead:

                       OVC.TumorID: 1552///Survival: 33///X0...alive...1...dead:

                       OVC.TumorID: 1578///Survival: 33///X0...alive...1...dead:

                        OVC.TumorID: 1590///Survival: 148///X0...alive...1...dea

                       OVC.TumorID: 1615///Survival: 13///X0...alive...1...dead:

                        OVC.TumorID: 1623///Survival: 147///X0...alive...1...dea

                       OVC.TumorID: 1665///Survival: 15///X0...alive...1...dead:

                        OVC.TumorID: 1674///Survival: 18///X0...alive...1...dead

                      OVC.TumorID: 1675///Survival: 34///X0...alive...1...dead:

                      OVC.TumorID: 1774///Survival: 22///X0...alive...1...dead:

                        OVC.TumorID: 1784///Survival: 78///X0...alive...1...dead

                       OVC.TumorID: 1834///Survival: 118///X0...alive...1...dead

                        OVC.TumorID: 1846///Survival: 142///X0...alive...1...dea

                        OVC.TumorID: 1877///Survival: 119///X0...alive...1...dea
```

OVC.TumorID: 1913///Survival: 32///X0...alive...1...dead:

OVC.TumorID: 1929///Survival: 134///X0...alive...1...dea

OVC.TumorID: 2046///Survival: 127///X0...alive...1...dea

OVC.TumorID: 2063///Survival: 16///X0...alive...1...dead:

OVC.TumorID: 2064///Survival: 27///X0...alive...1...dead: 1///

OVC.TumorID: 2075///Survival: 87///X0...alive...1...dea

OVC.TumorID: 2198///Survival: 91///X0...alive...1...dea

OVC.TumorID: 2204///Survival: 118///X0...alive...1...dea

OVC.TumorID: 2324///Survival: 98///X0...alive...1...dea

OVC.TumorID: 2419///Survival: 107///X0...alive...1...dead

OVC.TumorID: 2422///Survival: 20///X0...alive...1...dea

OVC.TumorID: 2424///Survival: 16///X0...alive...1...dead:

OVC.TumorID: 2465///Survival: 17///X0...alive...1...dead:

OVC.TumorID: 2476///Survival: 86///X0...alive...1...dead:

OVC.TumorID: 2479///Survival: 95///X0...alive...1...dead:

OVC.TumorID: 2505///Survival: 95///X0...alive...1...dead

OVC.TumorID: 2542///Survival: 36///X0...alive...1...dea

OVC.TumorID: 2573///Survival: 7///X0...alive...1...dead: 1

OVC.TumorID: 2673///Survival: 74///X0...alive...1...dead:

OVC.TumorID: 2739///Survival: 67///X0...alive...1...dead

OVC.TumorID: 2802///Survival: 24///X0...alive...1...dead:

OVC.TumorID: 2849///Survival: 23///X0...alive...1...dead:

OVC.TumorID: 2895///Survival: 9///X0...alive...1...dead:

OVC.TumorID: 2967///Survival: 22///X0...alive...1...dead

OVC.TumorID: 2981///Survival: 6///X0...alive...1...dead:

OVC.TumorID: 2999///Survival: 16///X0...alive...1...dead:

OVC.TumorID: 3018///Survival: 16///X0...alive...1...dead:

OVC.TumorID: 3090///Survival: 16///X0...alive...1...dead:

OVC.TumorID: 3102///Survival: 10///X0...alive...1...dead: 1

OVC.TumorID: 3107///Survival: 31///X0...alive...1...dead:

OVC.TumorID: 3142///Survival: 18///X0...alive...1...dead

OVC.TumorID: 860///Survival: 17///X0...alive...1...dead:

OVC.TumorID: 872///Survival: 185///X0...alive...1...dead:

OVC.TumorID: 922///Survival: 183///X0...alive...1...dea

OVC.TumorID: D1805///Survival: 9///X0...alive...1...dead:

OVC.TumorID: D1837///Survival: 83///X0...alive...1...dead:

OVC.TumorID: D1859///Survival: 110///X0...alive...1...dead

OVC.TumorID: D2098///Survival: 42///X0...alive...1...dead

OVC.TumorID: D2208///Survival: 2///X0...alive...1...dead: 0

OVC.TumorID: D2332///Survival: 27///X0...alive...1...dead

OVC.TumorID: D2342///Survival: 20///X0...alive...1...dead:

OVC.TumorID: D2358///Survival: 9///X0...alive...1...dead

OVC.TumorID: D2421///Survival: 12///X0...alive...1...dead

OVC.TumorID: D2432///Survival: 34///X0...alive...1...dea

OVC.TumorID: D2433///Survival: 49///X0...alive...1...dead:

OVC.TumorID: D2480///Survival: 34///X0...alive...1...dead:

OVC.TumorID: D2557///Survival: 62///X0...alive...1...dead:

OVC.TumorID: D2559///Survival: 5///X0...alive...1...dead:

OVC.TumorID: D2560///Survival: 91///X0...alive...1...dead:

OVC.TumorID: D2572///Survival: 37///X0...alive...1...dead

OVC.TumorID: D2575///Survival: 33///X0...alive...1...dead:

OVC.TumorID: D2576///Survival: 17///X0...alive...1...dead:

OVC.TumorID: D2581///Survival: 63///X0...alive...1...dead

OVC.TumorID: D2603///Survival: 42///X0...alive...1...dead:

OVC.TumorID: D2611///Survival: 2///X0...alive...1...dead:

OVC.TumorID: D2629///Survival: 36///X0...alive...1...dead

OVC.TumorID: D2640///Survival: 1///X0...alive...1...dead: 1

OVC.TumorID: D2648///Survival: 35///X0...alive...1...dead:

OVC.TumorID: D2668///Survival: 40///X0...alive...1...d

OVC.TumorID: D2689///Survival: 45///X0...alive...1...dead:

OVC.TumorID: D2691///Survival: 63///X0...alive...1...dead:

OVC.TumorID: D2700///Survival: 74///X0...alive...1...dead:

OVC.TumorID: D2726///Survival: 71///X0...alive...1...dead:

OVC.TumorID: D2727///Survival: 53///X0...alive...1...dead

OVC.TumorID: D2733///Survival: 55///X0...alive...1...dead:

OVC.TumorID: D2738///Survival: 68///X0...alive...1...dead:

OVC.TumorID: D2749///Survival: 24///X0...alive...1...dead:

OVC.TumorID: D2776///Survival: 10///X0...alive...1...dead:

OVC.TumorID: D2792///Survival: 16///X0...alive...1...dead:

OVC.TumorID: M1054///Survival: 101///X0...alive...1...dead: 0///As

OVC.TumorID: M1055///Survival: 13///X0...alive...1...dead: 0///Assig

OVC.TumorID: M120///Survival: 35///X0...alive...1...dead: 1///Ass

OVC.TumorID: M1241///Survival: 95///X0...alive...1...dead: 0///Assigne

OVC.TumorID: M1390///Survival: 46///X0...alive...1...dead:

OVC.TumorID: M1503///Survival: 53///X0...alive...1...dead: 1///Ass

OVC.TumorID: M1572///Survival: 22///X0...alive...1...dead: 1///Assi

OVC.TumorID: M17///Survival: 17///X0...alive...1...dead: 0///Assigned.

OVC.TumorID: M1891///Survival: 12///X0...alive...1...dead: 0///Assigned.Stage: 4

```
            OVC.TumorID: M2070///Survival: 65///X0...alive...1...dead: 0///Assigne
                OVC.TumorID: M2097///Survival: 58///X0...alive...1...dead: 0///A
              OVC.TumorID: M2184///Survival: 34///X0...alive...1...dead: 0///Assi
```

Value

An expression set

`PMID19318476` *Microarray analysis of early stage serous ovarian cancers shows profiles predictive of favorable outcome.*

Description

Although few women with advanced serous ovarian cancer are cured, detection of the disease at an early stage is associated with a much higher likelihood of survival. We previously used gene expression array analysis to distinguish subsets of advanced cancers based on disease outcome. In the present study, we report on gene expression of early-stage cancers and validate our prognostic model for advanced-stage cancers.Frozen specimens from 39 stage I/II, 42 stage III/IV, and 20 low malignant potential cancers were obtained from four different sites. A linear discriminant model was used to predict survival based upon array data.We validated the late-stage survival model and show that three of the most differentially expressed genes continue to be predictive of outcome. Most early-stage cancers (38 of 39 invasive, 15 of 20 low malignant potential) were classified as long-term survivors (median probabilities 0.97 and 0.86). MAL, the most differentially expressed gene, was further validated at the protein level and found to be an independent predictor of poor survival in an unselected group of advanced serous cancers (P = 0.0004).These data suggest that serous ovarian cancers detected at an early stage generally have a favorable underlying biology similar to advanced-stage cases that are long-term survivors. Conversely, most late-stage ovarian cancers seem to have a more virulent biology. This insight suggests that if screening approaches are to succeed it will be necessary to develop approaches that are able to detect these virulent cancers at an early stage.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Berchuck A, Iversen ES, Luo J, Clarke JP, Horne H, Levine D
  Laboratory: Berchuck, Lancaster 2009
  Contact information:
  Title: Microarray analysis of early stage serous ovarian cancers shows profile
  URL:
  PMIDs: 19318476

  Abstract: A 241 word abstract is available. Use 'abstract' method.
```

```
  Information is available on: preprocessing
  notes:
   platform_title:
      [HG-U133A] Affymetrix Human Genome U133A Array
   platform_shorttitle:
      Affymetrix HG-U133A
   platform_summary:
      hgu133a
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL96
   warnings:
      These samples are a subset of PMID17290060.
   version:
      2015-09-22 20:20:30

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-HUMISGF3A/M97935_MB_at
    (20967 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 20967 features, 42 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

      n  events  median 0.95LCL 0.95UCL
  42.00   22.00    2.79    2.30      NA

---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
D1462 D1805 D2171 D2208 D2247 D2332 D2432 D2480 D2559 D2560 D2575 D2576 D2611
    1     1     1     1     1     1     1     1     1     1     1     1     1
D2629 D2640 D2648 D2736 D2749 D2776 D2792 M1025 M1054 M1055  M120 M1241 M1572
    1     1     1     1     1     1     1     1     1     1     1     1     1
  M17 M1777 M1891 M2184 M2515 M2807 M3035  M337 M3484  M359 M4161  M444  M503
    1     1     1     1     1     1     1     1     1     1     1     1     1
M5668 M5775  M806
    1     1     1

sample_type:
tumor
```

```
   42

histological_type:
ser
 42

summarygrade:
high  low NA's
  24   17    1

summarystage:
early  late  NA's
    2    39     1

tumorstage:
   1    2    3    4 NA's
   1    1   29   10    1

substage:
   a    b    c NA's
   1    1   29   11

grade:
   1    2    3 NA's
   2   15   24    1

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  33.00   55.00   62.00   61.46   70.00   81.00       1

recurrence_status:
norecurrence   recurrence
           6           36

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   30.0   367.5   825.0  1105.0  1050.0  3420.0

vital_status:
deceased   living
      22       20

debulking:
   optimal suboptimal       NA's
        20         21          1

batch:
2004-03-09 2004-03-16 2004-04-20 2004-05-18 2004-05-21 2004-05-27 2004-06-22
        14          3          4          8          6          5          1
2004-06-23
         1
```

uncurated_author_metadata:

Tumor: D2560///NEW.Response: CR///SHORT.LONG: NA///AgeDx: 60///DateDx: 5/14/1996

Value

An expression set

`TCGA.RNASeqV2` *Integrated genomic analyses of ovarian carcinoma.*

Description

A catalogue of molecular aberrations that cause ovarian cancer is critical for developing and deploying therapies that will improve patients' lives. The Cancer Genome Atlas project has analysed messenger RNA expression, microRNA expression, promoter methylation and DNA copy number in 489 high-grade serous ovarian adenocarcinomas and the DNA sequences of exons from coding genes in 316 of these tumours. Here we report that high-grade serous ovarian cancer is characterized by TP53 mutations in almost all tumours (96%); low prevalence but statistically recurrent somatic mutations in nine further genes including NF1, BRCA1, BRCA2, RB1 and CDK12; 113 significant focal DNA copy number aberrations; and promoter methylation events involving 168 genes. Analyses delineated four ovarian cancer transcriptional subtypes, three microRNA subtypes, four promoter methylation subtypes and a transcriptional signature associated with survival duration, and shed new light on the impact that tumours with BRCA1/2 (BRCA1 or BRCA2) and CCNE1 aberrations have on survival. Pathway analyses suggested that homologous recombination is defective in about half of the tumours analysed, and that NOTCH and FOXM1 signalling are involved in serous ovarian cancer pathophysiology.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Integrated genomic analyses of ovarian carcinoma. Nature 20
  Laboratory: Cancer Genome Atlas Research Network 2011
  Contact information:
  Title: Integrated genomic analyses of ovarian carcinoma.
  URL:
  PMIDs: 21720365

  Abstract: A 179 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [RNASeqV2] Illumina HiSeq RNA sequencing
   platform_shorttitle:
      Illumina HiSeq RNA sequencing
   platform_summary:
      NA
   platform_manufacturer:
      Illumina
   platform_distribution:
      sequencing
   platform_accession:
      NA
   platform_technology:
      RNA sequencing
   version:
      2015-09-22 20:27:26

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: ?|100133144 ?|100134869 ... ZZZ3|26009 (20471 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
```

Details

```
assayData: 20471 features, 261 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)
```

```
   5 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
 256.00  143.00    3.62    3.19    4.03

---------------------------
Available sample meta-data:
---------------------------

alt_sample_name:
TCGA-04-1348-01A-01R-1565-13 TCGA-04-1357-01A-01R-1565-13
                           1                            1
TCGA-04-1362-01A-01R-1565-13 TCGA-04-1364-01A-01R-1565-13
                           1                            1
TCGA-04-1365-01A-01R-1565-13 TCGA-04-1514-01A-01R-1566-13
                           1                            1
TCGA-04-1519-01A-01R-1565-13 TCGA-09-0364-01A-02R-1564-13
                           1                            1
TCGA-09-0366-01A-01R-1564-13 TCGA-09-0367-01A-01R-1564-13
                           1                            1
TCGA-09-0369-01A-01R-1564-13 TCGA-09-1662-01A-01R-1566-13
                           1                            1
TCGA-09-1666-01A-01R-1566-13 TCGA-09-1667-01C-01R-1566-13
                           1                            1
TCGA-09-1668-01B-01R-1566-13 TCGA-09-1669-01A-01R-1566-13
                           1                            1
TCGA-09-1670-01A-01R-1566-13 TCGA-09-1673-01A-01R-1566-13
                           1                            1
TCGA-09-1674-01A-01R-1566-13 TCGA-09-2044-01B-01R-1568-13
                           1                            1
TCGA-09-2045-01A-01R-1568-13 TCGA-09-2048-01A-01R-1568-13
                           1                            1
TCGA-09-2051-01A-01R-1568-13 TCGA-09-2054-01A-01R-1568-13
                           1                            1
TCGA-09-2056-01B-01R-1568-13 TCGA-10-0928-01A-02R-1564-13
                           1                            1
TCGA-10-0936-01A-01R-1564-13 TCGA-13-0730-01A-01R-1564-13
                           1                            1
TCGA-13-0799-01A-01R-1564-13 TCGA-13-0800-01A-01R-1564-13
                           1                            1
TCGA-13-0801-01A-01R-1564-13 TCGA-13-0890-01A-01R-1564-13
                           1                            1
TCGA-13-0893-01B-01R-1565-13 TCGA-13-0897-01A-01R-1564-13
                           1                            1
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TCGA-24-1558 TCGA-24-1560 TCGA-24-1562      (Other)
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sample_type:
tumor
  261

histological_type:
ser
261

primarysite:
```

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other    ov
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summarygrade:
high  low NA's
 226   29    6

summarystage:
early  late  NA's
   18   242     1

tumorstage:
   2    3    4 NA's
  18  209   33    1

substage:
   b    c NA's
  16  211   34

grade:
   1    2    3    4 NA's
   1   28  225    1    6

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  34.00   51.00   58.00   58.84   66.00   87.00

pltx:
   n    y NA's
  17  215   29

tax:
   n    y NA's
  17  215   29

neo:
   n NA's
 232   29

days_to_tumor_recurrence:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    9.0   225.0   426.5   585.3   755.0  5480.0      19

recurrence_status:
norecurrence   recurrence
         123          138

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
    9.0   341.8   878.0  1018.0  1446.0  5480.0       5

vital_status:
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deceased   living     NA's 
     143      114        4 

site_of_tumor_first_recurrence:
locoregional   metastasis         NA's 
          82           56          123 

primary_therapy_outcome_success:
  completeresponse    partialresponse progressivedisease      stabledisease 
               147                 30                 15                 15 
              NA's 
                54 

debulking:
   optimal suboptimal       NA's 
       171         60         30 

percent_normal_cells:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  0.000   0.000   0.000   2.066   0.000  55.000       5 

percent_stromal_cells:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   0.00    5.00   10.00   11.43   15.00   70.00       4 

percent_tumor_cells:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   0.00   77.00   85.00   82.07   90.00  100.00       4 

uncurated_author_metadata:




age_at_initial_pathologic_diagnosis: 38///anatomic_organ_subdivision: Bilateral/

                                                                    age_at_initi

                                                                          age_at

                                                     age_at_initial_pathologic_di

                                              age_at_initial_pathologic_diagnosis

                                                  age_at_initial_pathologic_diagn

                                                                          age_at

                  age_at_initial_pathologic_diagnosis: 42///anatomic_organ_subd
```

```
age_at_initial_pathologic_diagnosis

age_at_i

age_at_initial_p

age_at_initial_pat

age_at_initial_patho

age_at_initia

age_at_initial_pathologic_diagnosis: 45///anatomic

age

age_at_initial_pathologic_diagnosis: 45///an

age_at_initial_patho

age_at_initial_path

age_at_initial_pathologic_diagno

age_at_initial_pathologic_diagnosis: 45///anatomic_organ_subdivisio

age_at_initial_pathologic_

age_at_initial_pathologic_diagnosis: 46///anatomic_organ_subdivisi

age_at_initial_pathologic_diagnosis:
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age_at_initial_pathologic_diagnc
age_at_initial_pathologic_diagnosis: 47///anatc
age_at_initi
age_at_initial_pathologic_diagnosis: 47///anatomic_
age_at_initial_pathologic_diagnosis: 48///
age
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age_at_initial_pathologic_
age_at_in
age_at_initial_pathologic_diagnosis: 49///anatom
age_at_initial_pathologic_diagnosis: 50///anatomic_org
age_at_initial_pathologic_dia
age_at_initial_pat
age_at_initial_pathologic_diagnosis: 50///anatomic_organ_subdivision: Left///bc
age_at_initial_pathologic_diagnosis: 50///ana
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age_at_initial_pathol

age_at_initial_pathologic_diagnosis: 51///anatomic_organ_subdivision: Bilatera

age_at_init

age_at_initial_pathologic_dia

age_at

age

age_at_initial_pathologic_diagnosis: 51///anat

age_at_initial_pathologic

age_at_initia

age_at_initial_pathologi

age_at_initial_pathologic_di

age_

age_at_initial_pathologic_diagnos

age_at_initial_pat

age_at_initial_pathologic_di

age_at_initial_pathologic_diagnosis: 53///anatomic_organ_

age_at_initial_pathologic_diagnosi

age_at_initial_pathologic_diagnosis: 53///anato

age_at_initial_pat

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                                                                              age_a
                                                                           age_at_ini

                                                                             age_at_i
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Value

An expression set

`TCGAOVARIAN` *Integrated genomic analyses of ovarian carcinoma.*

Description

A catalogue of molecular aberrations that cause ovarian cancer is critical for developing and deploying therapies that will improve patients' lives. The Cancer Genome Atlas project has analysed messenger RNA expression, microRNA expression, promoter methylation and DNA copy number in 489 high-grade serous ovarian adenocarcinomas and the DNA sequences of exons from coding genes in 316 of these tumours. Here we report that high-grade serous ovarian cancer is characterized by TP53 mutations in almost all tumours (96%); low prevalence but statistically recurrent somatic mutations in nine further genes including NF1, BRCA1, BRCA2, RB1 and CDK12; 113 significant focal DNA copy number aberrations; and promoter methylation events involving 168 genes. Analyses delineated four ovarian cancer transcriptional subtypes, three microRNA subtypes, four promoter methylation subtypes and a transcriptional signature associated with survival duration, and shed new light on the impact that tumours with BRCA1/2 (BRCA1 or BRCA2) and CCNE1 aberrations have on survival. Pathway analyses suggested that homologous recombination is defective in about half of the tumours analysed, and that NOTCH and FOXM1 signalling are involved in serous ovarian cancer pathophysiology.

Format

```
experimentData(eset):
Experiment data
  Experimenter name: Integrated genomic analyses of ovarian carcinoma. Nature 20
  Laboratory: Cancer Genome Atlas Research Network 2011
  Contact information:
  Title: Integrated genomic analyses of ovarian carcinoma.
  URL:
  PMIDs: 21720365

  Abstract: A 179 word abstract is available. Use 'abstract' method.
  Information is available on: preprocessing
  notes:
   platform_title:
      [HT_HG-U133A] Affymetrix HT Human Genome U133A Array
   platform_shorttitle:
      Affymetrix HT_HG-U133A
   platform_summary:
      hthgu133a
   platform_manufacturer:
      Affymetrix
   platform_distribution:
      commercial
   platform_accession:
      GPL3921
   warnings:
      The following samples are likely from specimens also used in GSE26712: TCG
A.13.0725, TCGA.13.0885, TCGA.13.0887, TCGA.13.0890, TCGA.13.0886, TCGA.13
.0714, TCGA.13.0727, TCGA.13.1817, TCGA.13.1499, TCGA.13.0883
   version:
      2015-09-22 20:25:15

featureData(eset):
An object of class 'AnnotatedDataFrame'
  featureNames: 1007_s_at 1053_at ... AFFX-M27830_M_at (21260 total)
  varLabels: probeset gene EntrezGene.ID best_probe
  varMetadata: labelDescription
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Details

```
assayData: 21260 features, 578 samples
Platform type:
Overall survival time-to-event summary (in years):
Call: survfit(formula = Surv(time, cens) ~ -1)

   21 observations deleted due to missingness
      n  events  median 0.95LCL 0.95UCL
 557.00  290.00    3.73    3.45    4.06

---------------------------
Available sample meta-data:
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TCGA-09-1672 TCGA-09-1673 TCGA-09-1674 TCGA-09-1675 TCGA-09-2043 TCGA-09-2044 
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           1            1            1            1            1            1 
TCGA-10-0936 TCGA-10-0937 TCGA-10-0938 TCGA-13-0714 TCGA-13-0717 TCGA-13-0720 
           1            1            1            1            1            1 
TCGA-13-0723 TCGA-13-0724 TCGA-13-0725      (Other) 
           1            1            1          479 

sample_type:
adjacentnormal          tumor 
             8            570 

histological_type:
 ser NA's 
 568   10 

primarysite:
other    ov  NA's 
    4   564    10 

summarygrade:
high  low NA's 
 480   75   23 
```

```
summarystage:
early  late  NA's 
   43   520    15 

tumorstage:
   1    2    3    4 NA's 
  16   27  436   84   15 

substage:
   b    c NA's 
  31  448   99 

grade:
   1    2    3    4 NA's 
   6   69  479    1   23 

age_at_initial_pathologic_diagnosis:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  26.00   51.00   59.00   59.70   68.25   89.00      10 

pltx:
   n    y NA's 
  19  492   67 

tax:
   n    y NA's 
  43  468   67 

neo:
   n NA's 
 511   67 

days_to_tumor_recurrence:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
    8.0   238.2   443.5   623.7   812.0  5480.0      56 

recurrence_status:
norecurrence   recurrence 
         279          299 

days_to_death:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
      8     349     881    1010    1446    5480      21 

vital_status:
deceased   living     NA's 
     290      270       18 

site_of_tumor_first_recurrence:
                locoregional locoregional_plus_metastatic 
                         153                            3 
                  metastasis                         NA's 
```

```
                         143                           279

primary_therapy_outcome_success:
  completeresponse    partialresponse progressivedisease      stabledisease
               318                 65                 41                 30
              NA's
               124

debulking:
   optimal suboptimal       NA's
       367        140         71

percent_normal_cells:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
  0.000   0.000   0.000   2.385   0.000  55.000      19

percent_stromal_cells:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00    5.00   10.00   12.85   20.00   70.00      25

percent_tumor_cells:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   0.00   75.00   85.00   80.64   90.00  100.00      22

batch:
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   9.00   13.00   17.00   18.55   22.00   40.00       1

uncurated_author_metadata:
                                              age_at_initial_pathologic_diagnosi







                                                                             age



                                                         age_at_initial_patholog

                                       age_at_initial_pathologic_diagnosis: 37//



age_at_initial_pathologic_diagnosis: 38///anatomic_organ_subdivision: Bilateral/

          age_at_initial_pathologic_diagnosis: 38///anatomic_organ_subdivision:

                                                                    age_at_initi
```

age_at

age_at_initial_pathologic_diagnosis: 39///

age_at_initial_pathologic_

age_at_initial_pathologic_di

age_at_initial_pathologic_diagnosis

age_at_initial_pathologic_diagnosis: 40///anatomic_organ

age_at_initial_pathologic_diagn

age_at

age_at_initial_pa

age_at_initial_pathologic_d

age_at_initial_pathologic_diagnosis

age_at_initial_pathologic_diagnosis: 42///anatomic_organ_subd

age_at_initial_

age_at_initial_pathologic_diagnosis: 42///anatomic_

age_at_initial_pat

age_at_initial_pathologic_diagnosis

age_at_

age_at_initial_pathologic_diagnosis

```
age_at_init
age_at_i
age_at_in



age_at_initial_pathologic_dia
age_at_initial_pathologic_diagnosis: 44///anatomi
age_at_initial_pathologic_di
age_at_initial_p
age_at_initial_pa
age_at_initial_pat



age_at_initial_patho


age_at_initia


age_at_initial_pathologic_diagnosis: 45///anatomic



age
age_at_initial_pathologic_diagnosis: 45///an
age_at_initial_patho
age_at_initial_path
age_at_initial_pathologic_diagno
```

age_at_initial_pathologic_diagnosis: 45///anatomic_organ_subdivisio

age_at_initial_pathologic_

age_at_initial_pathologic_diagnosis: 46///anatomic_organ_subdivis

age_at_initial_pathologic_diagnosis: 46///an

age_at_initial_pathologic_diagnosis:

age_at_initial_patholo

age_at_initial_pathologic_diagno

age_at_initial_pathologic_diagno

age_at_initial_pathologic_diagnosis: 47///anato

age_at_initi

age_at_initial_pathologic_diagnosis: 47///anatomic_

age_at_initial_pathologic_diagnosis: 48///

age_at_initial_pathologic_diagno

age_at_initial_pathologic

```
                                          age_at_initial_pathologic_diagnosis: 48///
```

```
duplicates:
   Length     Class      Mode 
      578 character character 
```

Value

An expression set